

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 19:21:17 ; Search time 27.3991 Seconds  
(without alignments)  
275.930 Million cell updates/sec

Title: US-10-044-896-3

Perfect score: 594  
Sequence: 1 DIQWQSPSLASVGRVT.....SMGIRTEGQTKVEIKRTV 114

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PTUS COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	509	85.7	130	1 US-08-137-117D-86	Sequence 86, Appl
2	509	85.7	130	2 US-08-436-717-86	Sequence 86, Appl
3	490	82.5	218	5 PCT-US96-13152-2	Sequence 2, Appl
4	487	82.0	109	3 US-09-157-370-3	Sequence 3, Appl
5	486	81.8	114	2 US-08-887-352B-9	Sequence 9, Appl
6	486	81.8	114	2 US-08-887-352B-10	Sequence 10, Appl
7	486	81.8	114	3 US-09-109-207C-10	Sequence 10, Appl
8	486	81.8	114	3 US-09-296-005-10	Sequence 10, Appl
9	486	81.8	114	4 US-09-920-171-10	Sequence 10, Appl
10	486	81.8	114	4 US-09-716-028-10	Sequence 10, Appl
11	486	81.8	114	4 US-10-113-996-10	Sequence 10, Appl
12	486	81.8	218	2 US-08-887-352B-13	Sequence 13, Appl
13	486	81.8	218	3 US-08-466-151-9	Sequence 9, Appl
14	486	81.8	218	3 US-09-109-207C-13	Sequence 13, Appl
15	486	81.8	218	3 US-09-296-005-13	Sequence 13, Appl
16	486	81.8	218	3 US-08-466-153B-9	Sequence 9, Appl
17	486	81.8	218	4 US-09-920-171-13	Sequence 13, Appl
18	486	81.8	218	4 US-09-802-096-9	Sequence 9, Appl
19	486	81.8	218	4 US-09-802-077-9	Sequence 9, Appl
20	486	81.8	218	4 US-09-716-028-13	Sequence 13, Appl
21	486	81.8	218	4 US-10-113-996-13	Sequence 13, Appl
22	483	81.3	114	3 US-09-109-207C-9	Sequence 9, Appl
23	483	81.3	114	3 US-08-286-005-9	Sequence 9, Appl
24	483	81.3	114	4 US-09-920-171-9	Sequence 9, Appl
25	483	81.3	114	4 US-09-716-028-9	Sequence 9, Appl
26	483	81.3	114	4 US-10-113-996-9	Sequence 9, Appl
27	483	81.3	240	4 US-09-192-854-2	Sequence 2, Appl

28	481	81.0	111	2 US-08-887-352B-7	Sequence 7, Appl
29	481	81.0	111	3 US-09-109-207C-7	Sequence 7, Appl
30	481	81.0	111	3 US-09-286-005-7	Sequence 7, Appl
31	481	81.0	111	4 US-09-920-171-7	Sequence 7, Appl
32	481	81.0	111	4 US-09-716-028-7	Sequence 7, Appl
33	481	81.0	111	4 US-10-113-996-7	Sequence 7, Appl
34	480.5	80.9	110	3 US-09-672-609-17	Sequence 17, Appl
35	480.5	80.9	110	4 US-09-025-403A-17	Sequence 17, Appl
36	477.5	80.4	110	3 US-09-672-609-15	Sequence 15, Appl
37	477.5	80.4	110	4 US-09-025-403A-15	Sequence 15, Appl
38	477	80.3	114	2 US-08-887-352B-8	Sequence 8, Appl
39	477	80.3	218	3 US-09-282-505-1	Sequence 1, Appl
40	477	80.3	218	3 US-09-054-255-1	Sequence 1, Appl
41	477	80.3	218	4 US-09-282-846-1	Sequence 1, Appl
42	477	80.3	218	4 US-09-680-145-1	Sequence 1, Appl
43	477	80.3	218	4 US-08-483-588-1	Sequence 1, Appl
44	476	80.1	131	3 US-08-579-378A-18	Sequence 18, Appl
45	475	80.0	214	2 US-07-934-373C-39	Sequence 39, Appl

# ALIGNMENTS

RESULT 1  
US-08-137-117D-86  
Sequence 86, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-86

Query Match 85.7%; Score 509; DB 1; Length 130;  
Best Local Similarity 90.1%; Pred. No. 2,7e-40;  
Matches 100; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRVTITTCRAQSVSTSSYSYMHMYOQKPGKAPKYLISYASNTLS 60  
DB 20 DIQMTQSPSSLSASVDGRVTITTCRAQSVSTSSYSYMHMYOQKPGKAPKYLISYASNTLS 79

QY 61 GVPSPRFGSGSGGTDFTLTSSLPEDPFAITYCOHSGWGIPTFGQTKVEIK 111  
DB 80 GVPSPRFGSGSGGTDFTLTSSLPEDPFAITYCOHSGWGIPTFGQTKVEIK 130

## RESULT 2

US-08-436-717-86  
Sequence 86, Application US/08436717  
Patent No. 5817790

## GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:

## CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 130 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-436-717-86

Query Match 85.7%; Score 509; DB 2; Length 130;  
Best Local Similarity 90.1%; Pred. No. 2,7e-40;  
Matches 100; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRVTITTCRAQSVSTSSYSYMHMYOQKPGKAPKYLISYASNTLS 60  
DB 20 DIQMTQSPSSLSASVDGRVTITTCRAQSVSTSSYSYMHMYOQKPGKAPKYLISYASNTLS 79

QY 61 GVPSPRFGSGSGGTDFTLTSSLPEDPFAITYCOHSGWGIPTFGQTKVEIK 111  
DB 80 GVPSPRFGSGSGGTDFTLTSSLPEDPFAITYCOHSGWGIPTFGQTKVEIK 130

## RESULT 3

PCT-US96-13152-2  
Sequence 2, Application PC/TUS9613152

## GENERAL INFORMATION:

APPLICANT: Martin, Ulrich, et al.  
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Felle & Lynch  
ADDRESSER: Attn: Norman D. Hanson  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/13152  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953  
FILING DATE: 27-Dec-95  
APPLICATION NUMBER: EP 95 112 895.8  
FILING DATE: 17-Aug-95  
APPLICATION NUMBER: EP 95 114 969.9  
FILING DATE: 19-Sep-95  
ATTORNEY/AGENT INFORMATION:

NAME: Norman D. Hanson

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
PCT-US96-13152-2

Query Match 82.5%; Score 490; DB 5; Length 218;  
Best Local Similarity 86.0%; Pred. No. 2,9e-38;  
Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRVTITTCRAQSVSTSSYSYMHMYOQKPGKAPKYLISYASNTLS 60  
DB 1 DIQMTQSPSSLSASVDGRVTITTCRAQSVSTSSYSYMHMYOQKPGKAPKYLISYASNTLS 60

QY 61 GVPSPRFGSGSGGTDFTLTSSLPEDPFAITYCOHSGWGIPTFGQTKVEIKRTV 114  
DB 61 GVPSPRFGSGSGGTDFTLTSSLPEDPFAITYCOHSGWGIPTFGQTKVEIKRTV 114

RESULT 4  
US-09-157-370-3  
; Sequence 3, Application US/09157370A  
; Patent No. 6262238  
; GENERAL INFORMATION:  
; APPLICANT: STEIRPE, Boris  
; APPLICANT: STEINBACHER, Stefan  
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES  
; FILE REFERENCE: P9341-8072  
; CURRENT APPLICATION NUMBER: US/09/157,370A  
; EARLIER FILING DATE: 1998-09-21  
; EARLIER APPLICATION NUMBER: 08/765,179  
; EARLIER FILING DATE: 1997-01-14  
; EARLIER APPLICATION NUMBER: PCT/EP95/02626  
; EARLIER FILING DATE: 1995-07-06  
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7  
; EARLIER FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-157-370-3

Query Match 82.0%; Score 487; DB 3; Length 109;  
Best Local Similarity 85.8%; Pred. No. 2.5e-38;  
Matches 97; Conservative 5; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISYASNLES 60  
Db 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISYASNLES 56

Qy 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 113  
Db 57 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 109

RESULT 5  
US-08-887-352B-9  
; Sequence 9, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids

TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-9

Query Match 81.8%; Score 486; DB 2; Length 114;  
Best Local Similarity 86.0%; Pred. No. 3.2e-38;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISYASNLES 60  
Db 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISYASNLES 60

Qy 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 114  
Db 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 114

RESULT 6  
US-08-887-352B-10  
; Sequence 10, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-10

Query Match 81.8%; Score 486; DB 2; Length 114;  
Best Local Similarity 86.0%; Pred. No. 3.2e-38;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISYASNLES 60  
Db 1 DIQMTSPSSLSASVGVGRVITTCRASQSVSTSSYNNHWYQKRGKAPKYLISYASNLES 60

Qy 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 114  
Db 61 GVPSRFSGSGSGTDFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 114

RESULT 7  
US-09-109-207C-10  
; Sequence 10, Application US/09109207C  
; Patent No. 6172213

```
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
/ FILE REFERENCE: P1123R1
/ CURRENT APPLICATION NUMBER: US/09/109,207C
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/051,554
/ PRIOR FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-10
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```
Query Match      81.8%; Score 486; DB 3; Length 114;
Best Local Similarity 86.0%; Pred. No. 3,2e-38;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNTLS 60
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Db 1 DIQMTSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGDTFTLTISLQPEDPATYCCQSHEDPYTFQGTKEIKRTV 114
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RESULT 8
US-09-296-005-10
/ Sequence 10, Application US/09296005
/ Patent No. 6290957
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
/ FILE REFERENCE: P1123C1r
/ CURRENT APPLICATION NUMBER: US/09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ EARLIER APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ NUMBER OF SEQ ID NOS: 26
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-10
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```
Query Match      81.8%; Score 486; DB 3; Length 114;
Best Local Similarity 86.0%; Pred. No. 3,2e-38;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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Db 1 DIQMTSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGDTFTLTISLQPEDPATYCCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGDTFTLTISLQPEDPATYCCQSHEDPYTFQGTKEIKRTV 114
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RESULT 9
US-09-920-171-10
/ Sequence 10, Application US/09920171
/ Patent No. 6682735
/ GENERAL INFORMATION:
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```
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
/ FILE REFERENCE: P1123C2US
/ CURRENT APPLICATION NUMBER: US/09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-10
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Query Match      81.8%; Score 486; DB 4; Length 114;
Best Local Similarity 86.0%; Pred. No. 3,2e-38;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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Db 1 DIQMTSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGDTFTLTISLQPEDPATYCCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGDTFTLTISLQPEDPATYCCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

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RESULT 10
US-09-716-028-10
/ Sequence 10, Application US/09716028
/ Patent No. 6723833
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
/ FILE REFERENCE: P1123R1
/ CURRENT APPLICATION NUMBER: US/09/716,028
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: US 09/109,207
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/051,554
/ PRIOR FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-716-028-10
```

```
Query Match      81.8%; Score 486; DB 4; Length 114;
Best Local Similarity 86.0%; Pred. No. 3,2e-38;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNTLS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGDTFTLTISLQPEDPATYCCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVPSRFGSGSGGDTFTLTISLQPEDPATYCCQSHEDPYTFQGTKEIKRTV 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 11
```

US-10-113-996-10  
; Sequence 10, Application US/1011396  
; Patent No. 6761889  
; GENERAL INFORMATION:  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies  
; FILE REFERENCE: P1123CJUS  
; CURRENT APPLICATION NUMBER: US/10/113, 996  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: US 08/887,352  
; PRIOR FILING DATE: 1997-07-02  
; PRIOR APPLICATION NUMBER: US 09/296, 005  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: US 09/920, 171  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 10  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-10-113-996-10  
Query Match 81.8%; Score 486; DB 4; Length 114;  
Best Local Similarity 86.0%; Pred. No. 3,2e-38;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
QY 1 DIQWTQSSLSASVSGRVITTCRASQSVSTSSYSYMWYQKKGKAPKVLISYASNI 60  
DB 1 DIQWTQSSLSASVSGRVITTCRASQSVSDYDGSYMWYQKKGKAPKVLISYASNI 60  
QY 61 GVPSRFSGSGGTFTLTISLSQPEDPATYTCQHSWGIPTFGGTVEIKRTV 114  
DB 61 GVPSRFSGSGGTFTLTISLSQPEDPATYTCQSHEDPYTFGGTVEIKRTV 114  
RESULT 12  
US-08-887-352B-13  
; Sequence 13, Application US/0887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/952-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-13  
Query Match 81.8%; Score 486; DB 2; Length 218;  
Best Local Similarity 86.0%; Pred. No. 6,8e-38;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;  
QY 1 DIQWTQSSLSASVSGRVITTCRASQSVSTSSYSYMWYQKKGKAPKVLISYASNI 60  
DB 1 DIQWTQSSLSASVSGRVITTCRASQSVSDYDGSYMWYQKKGKAPKVLISYASNI 60  
QY 61 GVPSRFSGSGGTFTLTISLSQPEDPATYTCQHSWGIPTFGGTVEIKRTV 114  
DB 61 GVPSRFSGSGGTFTLTISLSQPEDPATYTCQSHEDPYTFGGTVEIKRTV 114  
RESULT 13  
US-08-466-151-9  
; Sequence 9, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/952-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-9  
Query Match 81.8%; Score 486; DB 3; Length 218;



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OM protein - protein search, using sw model

Run on: December 29, 2004, 18:59:15 ; Search time 117.425 Seconds  
(without alignments)  
348.266 Million cell updates/sec

Title: US-10-044-896-3

Perfect score: 594  
Sequence: 1 DIQWTQSPSSLSASVGRVT.....SMGIPTFGQCTKYIKRTV 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq.23Sep04:\*

1: geneSeqp1980s:.\*  
2: geneSeqp1990s:.\*  
3: geneSeqp2000s:.\*  
4: geneSeqp2001s:.\*  
5: geneSeqp2002s:.\*  
6: geneSeqp2003as:.\*  
7: geneSeqp2003bs:.\*  
8: geneSeqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	100.0	114	5	AAE28148
2	501	84.3	111	2	AAE85242
3	494	83.2	118	5	AAW49204
4	493	83.0	132	2	AAW22842
5	490	82.5	218	5	AAW13563
6	489	82.3	108	6	ABP96011
7	489	82.3	108	8	ADL92462
8	489	82.3	238	3	AAW90930
9	489	82.3	238	5	ABW74899
10	488	82.2	238	5	AAW90932
11	488	82.2	238	5	ABW74901
12	488	82.2	240	4	AAW45995
13	486	81.8	114	2	AAW13922
14	486	81.8	114	2	AAW95654
15	486	81.8	114	2	AAW95655
16	486	81.8	114	2	AAW76944
17	486	81.8	114	8	ADN07031
18	486	81.8	218	4	AAW95658
19	486	81.8	218	4	AAW85200
20	486	81.8	218	4	AAW76847
21	486	81.8	218	8	ADN07034
22	486	81.8	240	4	AAW45996
23	485	81.6	238	5	AAW90931
24	485	81.6	238	5	ABW74900
25	484	81.5	233	8	ADL93655

26	484	81.5	240	4	AAW46010	AAW46010 Human MUC
27	483	81.3	108	6	ABP96009	ABP96009 HSA anti-b
28	483	81.3	108	7	ADL93345	ADL93345 VL chain
29	483	81.3	108	8	ADL92386	ADL92386 Anti-HSA
30	483	81.3	108	8	ADW36372	ADW36372 Intracell
31	483	81.3	114	4	AAW76943	AAW76943 Variable
32	483	81.3	114	8	ADN07030	ADN07030 Anti-IGF
33	483	81.3	219	8	ADN07065	ADN07065 F(ab)-pha
34	483	81.3	240	2	AAW02472	AAW02472 A single
35	483	81.3	240	4	AAW46007	AAW46007 Human MUC
36	483	81.3	240	4	AAW46038	AAW46038 Human Tr
37	483	81.3	240	4	AAW46008	AAW46008 Human MUC
38	483	81.3	240	4	AAW46005	AAW46005 Human MUC
39	483	81.3	240	4	AAW45994	AAW45994 Human MUC
40	483	81.3	240	6	ABP95997	ABP95997 Human ser
41	483	81.3	240	6	ABJ38594	ABJ38594 Hepatitis
42	483	81.3	240	6	ADL92369	ADL92369 Human pha
43	483	81.3	108	6	ABP96010	ABP96010 HSA anti-b
44	482	81.1	108	8	ADL92461	ADL92461 Single do
45	482	81.1	108	8	ADL92461	ADL92461 Single do

#### ALIGNMENTS

RESULT 1	AAE28148	AAE28148 standard; protein, 114 AA.
XX	AAE28148;	
AC		
XX		
DT	27-DEC-2002	(first entry)
XX		
DE	Humanised 9F3 version 13 (V13) light chain variable domain.	
XX		
KW	Human; interferon alpha; IFNalpha; insulin-dependent diabetes mellitus;	
KW	autoimmune disease; systemic lupus erythematosus; autoimmune thyroiditis;	
KW	antibody therapy; immunosuppressive; antiinflammatory; dermatological;	
KW	9F3 monoclonal antibody; light chain variable domain.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	Region	24..38
FT	Region	/note= "Complementarity determining region 1 (CDR1)"
FT	Region	54..60
FT	Region	/note= "Complementarity determining region 2 (CDR2)"
FT	Region	93..102
FT	Region	/note= "Complementarity determining region 3 (CDR3)"
XX		
PD	29-AUG-2002.	
XX		
PE	29-JAN-2002; 2002WO-US002709.	
XX		
PR	22-FEB-2001; 2001US-0270775P.	
PR	09-JAN-2002; 2002US-00044896.	
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Chuntarapai A, Kim JK, Presta LG, Stewart T;	
XX		
DR	WPI; 2002-682767/73.	
XX		
PT	New anti-interferon alpha monoclonal antibody, 9F3, useful for treating	
PT	autoimmune diseases e.g. insulin-dependent diabetes mellitus, systemic	
PT	lupus erythematosus and autoimmune thyroiditis.	
XX		
PS	Disclosure; Page 97; 100p; English.	
XX		
CC	The present invention relates to novel anti-interferon alpha (IFNalpha)	

Query Match	100.0%	Score 594	DB 5	Length 114
Best Local Similarity	100.0%	Pred. No. 2.9e-32		
Matches 114	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	DIDMTQSSSSISASVGRDVTTCRASQSVSYSSVMYQOKPEKAPKVLISVSNLES	60	
DB	1	DIQMTQSSSSISASVGRDVTTCRASQSVSYSSVMYQOKPEKAPKVLISVSNLES	60	
QY	61	GVPRPFGSSGSGTFTLTITSSLOPEDFATYYCOHSMGIPRTFGQTKYIKRTV	114	
DB	61	GVPRPFGSSGSGTFTLTITSSLOPEDFATYYCOHSMGIPRTFGQTKYIKRTV	114	
RESULT 2				
AA085242				
ID	AA085242	standard; protein; 111 AA.		
XX	AA085242;			
XX	09-APR-1996	(first entry)		
DE		Humanised antibody variable light chain region (VZV HuV).		
KM	Antibody; varicella zoster virus; Ab; VSV; treatment; prevention;			
KM	Infection; detection; isolation; monoclonal antibody; MAD; mimetic;			
KM	humanised; murine; heavy chain; light chain; variable region; CDR; NEMM;			
XX	REI.			
OS	Synthetic.			
XX	WO9531546-A1.			
XX	23-NOV-1995.			
XX	28-APR-1995;	95WO-US005305.		
XX	28-APR-1994;	94US-00234133.		
PA	(SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.			
XX	Moss MT; Wallace TP; Carr FU; Harris WJ;			
DR	WPI; 1996-010932/01.			
PT	Varicella zoster virus gpII antibody with humanised variable region -			
PT	infections.			
XX	Claim 7; Page 31; 58pp; English.			
XX	Antibodies (Ab) comprising a humanised variable region specifically			
CC	binding to a varicella zoster virus (VZV) can be used to treat or prevent			
CC	VZV infection. They may optionally be attached to a therapeutic agent.			
CC	They may also be used, when labelled, to detect VZV particles and			
CC	infected cells in blood; for the removal/neutralisation of infectious			
CC	VZV in blood; for the selection/ isolation of human monoclonal Abs and			
CC	for the design of (non-) peptide mimetics with similar diagnostic and			
CC	therapeutic uses. The variable region CDR portion is derived from murine			
CC	Ab 206 and the heavy and light chain variable region frameworks are NEMM			

CC		and REE respectively.	The framework may include at least one mutation	
CC		that improves binding specificity or affinity.	The heavy and light chain variable regions are preferably (VZVHu-VH,-YAKPILIS,-VAITLY,-YHKVRSE or -VHS) and VZVHuVK respectively	
XX	SQ	Sequence 111 AA;		
Query Match	84.3%;	Score 501;	DB 2; Length 111;	
Best Local Similarity	86.3%;	Pred. No. 4e-26;	Mismatches 9; Indels 0; Gaps 0;	
Matches	98;	Conservative	4; Mismatched	
Oy		1 DIOMTGPSSLSASVGGRVTTCRASOSVSSTSYVMWYOOKRGKAPKVLIYSASNLES 60    :   ::       : 1 DIGLTGSPSSLASAVGDRVTTCTCASSVETSGSYYHWYOQRKGKA PKLIIYASNLBS 60  Db      61 GVPSRFSGSGGTDFLTTLISLGPEDPATYYYCOHSHWGIPRTFGGVYEIK 111 61 GVPSRFSGSGGTDFLTTLISLGPEDIATYYYCQHRELPTFGGVYEIK 111		
RESULT 3				
ID	AAM49204			
AC	AAM49204	standard; protein; 218 AA.		
XX				
DT	29-AUG-2003	(revised)		
DT	28-JUN-2002	(first entry)		
DE		Humanised monoclonal antibody sc8 (huSc8) light chain.		
KM		Monoclonal antibody; mAb; humanised; murine; mouse; Sc8; huSc8; light chain; anti-CD145; CD145-antibody complex; 3D structure; three dimensional structure; drug design; drug discovery; activated T cell; CD40 interaction; T cell dependent immune response; agonist; antagonist; immune response; inflammatory response; autoimmune disease; allergy; inhibitor response; organ graft rejection; B cell cancer; Alzheimer's disease; multiple sclerosis; antinflammatory; immunosuppressive; antiallergic; cytostatic; dermatological; antiasthmatic; nootropic; neuroprotective; antiarteriosclerotic; antiviral; antidabetic; cardiant; antischaemic; vasodilator; antineumatic; antiarthritic; angioprotactic; immunomodulator; antibody; complementarity determining region; CDR; protein co-ordinate data. XX XX OS Mus sp. OS Homo sapiens. OS Chimeric. XX FH Key Location/Qualifiers FH Region 1..215 FT /note= "Forms part of the crystal of the invention" FT FT 21..38 FT /label= CDR1 FT /note= "Complementarity determining region 1" FT 31..32 FT /note= "Binds to CD145 (AAM49202)" FT 36 FT /note= "Binds to CD145 (AAM49202)" FT Binding-site FT 54..60 FT /label= CDR2 FT /note= "Complementarity determining region 2" FT FT 93..101 FT /label= CDR3 FT /note= "Complementarity determining region 3" FT 95..96 FT /note= "Binds to CD145 (AAM49202)" FN WO200218445-A2. PN PD 07-MAR-2002. PF 31-AUG-2001; 2001WO-US027352. XX		



PR 01-SEP-2000; 2000US-0229933P.  
PR 16-MAR-2001; 2001US-0276452P.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
PI Karpueas M, Hsu Y, Taylor FR, Zheng Z;  
XX  
DR WPI; 2002-329760/36.  
XX  
PT Crystal comprising a CD154 polypeptide complexed with an anti-CD154  
PT antibody, or its antigen binding fragment, useful for designing drugs for  
PT the treatment of an autoimmune disease, an allergy, multiple sclerosis  
PT and Alzheimer's disease.  
XX  
XX  
PS Example 1; Fig 8; 470pp; English.  
XX  
XX The invention relates to a crystal comprising a CD145 polypeptide in  
CC complex with an anti-CD45 antibody or its antigen-binding fragment, and  
CC the structure coordinates of such a crystal. In particular, the crystal  
CC comprises human CD145 (AAW49202) and a humanised version of the murine  
CC monoclonal antibody 5c8 (hu5c8; AAW49203, AAW49204). CD145, also known as  
CC CD40L, gp39, T-BAM, 5c8 antigen, CD40CR and TRAP) is a 32 kD type II  
CC membrane glycoprotein which is transiently expressed on activated T  
CC cells. It interacts with CD40 which is expressed on mature B cells,  
CC macrophages, dendritic cells, fibroblasts and activated endothelial  
CC cells. This CD40:CD145 interaction is required for T cell-dependent  
CC antibody responses, type I T-helper cell responses, and nitric oxide (NO)  
CC production by macrophages. NO mediates many of the pro-inflammatory  
CC activities of macrophages, and disruption of the CD40:CD145 interaction  
CC via the use of an anti-CD145 antibody has been shown to reduce the  
CC symptoms of autoimmune and inflammatory conditions. The crystal structure  
CC of the invention can be used to determine the three dimensional structure  
CC of the CD145:anti-CD145 antibody complex, and thereby provide information  
CC about this interaction which may be of use in designing non-antibody  
CC CD145 agonists and antagonists which modulate the CD40:CD145 interaction.  
CC Such compounds may be used in the treatment of an unwanted immune  
CC response, an unwanted inflammatory response, an autoimmune disease, an  
CC allergy, an inhibitor response to a therapeutic agent, rejection of a  
CC donor organ, or a B cell cancer. They may be specifically be used to  
CC treat systemic lupus erythematosus, lupus nephritis, lupus neuritis,  
CC asthma, chronic obstructive pulmonary disease (COPD), bronchitis,  
CC emphysema, multiple sclerosis, uveitis, Alzheimer's disease, traumatic  
CC spinal cord injury, stroke, atherosclerosis, coronary restenosis,  
CC ischaemic congestive heart failure, cirrhosis, hepatitis C, diabetic  
CC neuropathy, glomerulonephritis, osteoarthritis, rheumatoid arthritis,  
CC psoriasis, atopic dermatitis, systemic sclerosis, radiation-induced  
CC fibrosis, Crohn's disease, ulcerative colitis, multiple myeloma and  
CC cachexia. Sequences AAW49203 and AAW49204 represent, respectively, the  
CC heavy and light chains of the humanised version of the murine monoclonal  
CC antibody 5c8 (hu5c8). (Updated on 29-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 218 AA;  
Query Match 83.2%; Score 494; DB 5; Length 218;  
Best Local Similarity 79.8%; Pred. No. 2e-25;  
Matches 91; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
QY 1 DIQWTGSPSSLSASVGRVITTCRASQSVSTSSYSYMHYQOKRGKAPKVLISYASNL60  
Db 1 DIVLTGSPATLSVGPGRATISCRASQSVSSSTYSYMHYQOKRGKAPKVLISYASNL60  
QY 61 GVPSRFSGSSGNDFTLTISLQPEDPATYTCQHSKGIPTFGGTVEIKRTV 114  
Db 61 GVPSRFSGSSGNDFTLTISLQPEDPATYTCQHSWEIPTFGGTVEIKRTV 114  
RESULT 4  
ID AAW22842 standard; protein: 132 AA.  
AC AAW22842;  
XX  
DT 12-SEP-1997 (first entry)

XX  
DE Human anti-tumour antigen antibody light chain variable region.  
XX  
KW Human; tumour antigen; cancer; monoclonal; antibody; light chain;  
KW variable region; medicine; pharmacology; biochemistry; CDR;  
KW complementarity determining region.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT /label= sig\_peptide  
FT Peptide 23..132  
FT /label= mat\_peptide  
FT Region 46..56  
FT /label= CDR\_1  
FT Region 72..78  
FT /label= CDR\_2  
FT Region 111..119  
FT /label= CDR\_3  
XX  
XX JP09100300-A.  
XX  
XX 15-APR-1997.  
XX  
XX 03-OCT-1995; 95JP-00278266.  
XX  
XX 03-OCT-1995; 95JP-00278266.  
XX  
XX 03-OCT-1995; 95JP-00278266.  
XX  
XX (HAGI/) HAGIWARA Y.  
XX  
XX WPI: 1997-276726/25.  
XX  
XX N-PSDB; AAT75423.  
XX  
XX Anticancer human monoclonal antibody variable region sequences - and  
XX related DNA and RNA.  
XX  
PS Claim 9; Page 11; 14pp; Japanese.  
XX  
XX The present sequence is a human anti-tumour antigen monoclonal antibody  
XX (Mab) light chain variable region, useful in medicine, pharmacology and  
XX biochemistry. The isotype of a Mab secreted by the human/human hybridoma  
XX HT was determined to be mu and kappa. Human Mab was purified, and the  
XX antigen recognised by human Mab C1N-1gM identified by western blotting  
XX  
SQ Sequence 132 AA;  
Query Match 83.0%; Score 493; DB 2; Length 132;  
Best Local Similarity 85.1%; Pred. No. 1.6e-25;  
Matches 97; Conservative 8; Mismatches 5; Indels 4; Gaps 1;  
QY 1 DIQWTGSPSSLSASVGRVITTCRASQSVSTSSYSYMHYQOKRGKAPKVLISYASNL60  
Db 23 DIQWTGSPSSLSASVGRVITTCRASQSVSTSSYSYMHYQOKRGKAPKVLISYASNL60  
QY 61 GVPSRFSGSSGNDFTLTISLQPEDPATYTCQHSKGIPTFGGTVEIKRTV 114  
Db 79 GVPSRFSGSSGNDFTLTISLQPEDPATYTCQHSYSTPOTFGGTVEIKRTV 132  
RESULT 5  
ID AAW13563 standard; protein: 218 AA.  
AC AAW13563;  
XX  
XX  
DT 17-OCT-2003 (revised)  
DT 03-JUN-1997 (first entry)  
XX  
XX Humanised anti-L-selectin antibody HuDreg 55 light chain.  
XX  
XX L-selectin; humanised antibody; HuDreg 55; acute organ damage;  
KW organ failure; poly-trauma; haemorrhagic-traumatic shock.

```

XX OS Mus; sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX PN WO9706822-A1.
XX PD 27-FEB-1997.
XX PD 27-FEB-1997.
XX PF 14-AUG-1996; 96WO-US013152.
XX PR 17-AUG-1995; 95EP-00112895.
XX PR 19-SEP-1995; 95EP-00114696.
XX PR 27-DEC-1995; 95US-00578953.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PA (BOEF) BOEHRINGER MANNHEIM GMBH.
XX PI Haselbeck A, Schumacher G, Co M, Martin U;
XX PI WPI; 1997-165036/15.
XX DR N-PSDB; AAT61280.
XX PT Using anti-selectin antibody to prevent acute organ damage and multiple
XX PT organ failure - during extracorporeal circulation or following
XX PT polytrauma, e. g. haemorrhagic-traumatic shock.
XX PS Disclosure; Page 32-33; 52pp; English.
XX CC Humanised anti-L-selectin antibody Hudreg 55 comprises 2 light chains
XX CC each having the sequence given in AAM13563 and 2 heavy chains each having
XX CC the sequence given in AAM13564. These are encoded by the cDNA clones
XX CC given in AAT61280 and AAT61281. Hudreg 55 can be used to prevent multiple
XX CC organ failure associated with polytrauma and for the prevention of acute
XX CC organ damage associated with extracorporeal blood circulation. The
XX CC antibody inhibits interaction between the carbohydrate-recognising domain
XX CC of the selectin and the corresponding cell surface receptor. (Updated on
XX CC 17-OCT-2003 to standardise OS field)
XX SQ Sequence 218 AA;

Query Match 82.5%; Score 490; DB 2; Length 218;
Best Local Similarity 86.0%; Pred. No. 3.7e-25;
Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSVTSYVMHWYQOKRGA PKVLISYASNTLS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSVTDGSDYNNMWYQOKRGA PKVLISYASNTLS 60
QY 61 GVSRRFSGSGSGTDFTLTISSLQPEDPATYVCOHSGVIRPTFGQGTKEIKRTV 114
DB 61 GVSRRFSGSGSGTDFTLTISSLQPEDPATYVCOQSNMDPMTFGQGTKEIKRTV 114

```

RESULT 6  
ADL92462  
ID ADL92462 standard; protein; 108 AA.

```

XX AC ADL92462;
XX DT 01-MAY-2003 (first entry)
XX DE HSA antibody related V kappa chain E5sd.
XX DE HSA antibody related V kappa chain E5sd.
XX KW Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV;
XX KW anti-inflammatory; antianemic; immunosuppressive; neuroprotective;
XX KW dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia;
XX KW inflammation; autoimmune disorder; multiple sclerosis; Crohn's disease;
XX KW myasthenia gravis.
XX OS Homo sapiens.
XX OS Synthetic.

```

```

PN WO2003002609-A2.
XX PD 09-JAN-2003.
XX PF 28-JUN-2002; 2002WO-GB003014.
XX PR 28-JUN-2001; 2001GB-00015841.
XX PA (MED1-) MEDICAL RES COUNCIL.
XX PI Winter G, Ignatovich O, Tomlinson I;
XX PI WPI; 2003-210246/20.
XX DR Dual-specific ligand having immunoglobulins with binding specificity to
XX PT different antigens or epitopes, useful for treating, preventing or
XX PT diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
XX PT myasthenia gravis.
XX PS Example 1; Fig 3; 84pp; English.
XX CC The present invention describes a dual-specific ligand (I) comprising:
XX CC (a) a first single immunoglobulin variable domain with a binding
XX CC specificity to a first antigen or epitope; and (b) a second complementary
XX CC immunoglobulin single variable domain with a binding activity to a second
XX CC antigen or epitope. The binding domains are mutually complementary, and
XX CC the first and second domains lack mutually complementary domains that
XX CC share the same specificity. (I) has cytostatic, anti-HIV, antianemic,
XX CC anti-inflammatory, immunosuppressive and neuroprotective activities. The
XX CC dual-specific ligand is useful for treating, preventing or diagnosing
XX CC diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,
XX CC inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's
XX CC disease or myasthenia gravis). The dual-specific ligand may be used to
XX CC recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is
XX CC also useful for monitoring the efficacy of drugs, as well as for
XX CC monitoring toxicity. The present sequence represents a human serum
XX CC albumin (HSA) related antibody V kappa sequence, which is used in an
XX CC example from the present invention

```

SQ Sequence 108 AA;

Query Match 82.3%; Score 489; DB 6; Length 108;  
Best Local Similarity 85.7%; Pred. No. 2.4e-25;  
Matches 96; Conservative 6; Mismatches 6; Indels 4; Gaps 1;

```

QY 1 DIQMTQSPSSLSASVGRVTITCRASQSVTSYVMHWYQOKRGA PKVLISYASNTLS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSVS---STLNMWYQOKRGA PKVLISYASNTLS 56
QY 61 GVSRRFSGSGSGTDFTLTISSLQPEDPATYVCOHSGVIRPTFGQGTKEIKR 112
DB 57 GVSRRFSGSGSGTDFTLTISSLQPEDPATYVCOQNMWLPPTFGQGTKEIKR 108

```

RESULT 7  
ADL92462  
ID ADL92462 standard; protein; 108 AA.

```

XX AC ADL92462;
XX DT 20-MAY-2004 (first entry)
XX DE Single domain antibody-related light chain variable region E5sd protein.
XX DE Single domain antibody-related light chain variable region E5sd protein.
XX KW immunoglobulin single variable domain; cytostatic; anti-inflammatory;
XX KW antithrombotic; antithrombotic; antiallergic; antibacterial;
XX KW virucide; immunosuppressive; antidiabetic; neuroprotective; muscular;
XX KW dermatological; gene therapy; inflammatory; rheumatoid arthritis; asthma;
XX KW Crohn's disease; allergic hypersensitivity; bacterial; viral infection;
XX KW autoimmune disorder; type I diabetes; multiple sclerosis;
XX KW myasthenia gravis; systemic lupus erythematosus; cancer;
XX KW light chain variable region; human; E5sd.

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OS Unidentified.  
 XX  
 XX WO004003019-A2.  
 XX  
 XX 08-JAN-2004.  
 XX  
 XX 30-JUN-2003; 2003WO-GB002804.  
 XX  
 XX 28-JUN-2002; 2002WO-GB003014.  
 XX 27-DEC-2002; 2002GB-00030202.  
 XX  
 XX (DOMA-) DOMANTIS LTD.  
 XX  
 XX Walter G, Tomlinson I, Ignatovich O, Holt L, De Angelis E;  
 XX WPI; 2004-142855/14.  
 XX  
 XX New dual-specific ligands, useful in drug discovery and development, or  
 XX for diagnosing, preventing or treating a disease, such as cancer,  
 XX autoimmune disease, or inflammatory disease, including rheumatoid  
 XX arthritis or asthma.  
 XX  
 XX Example 1; Fig 3; 174pp; English.  
 XX  
 XX The invention relates to a novel dual-specific ligand comprising a first  
 XX immunoglobulin single variable domain having a binding specificity to a  
 XX first epitope or antigen and a second complementary immunoglobulin single  
 XX variable domain having a binding activity to a second epitope or antigen.  
 XX The ligand of the invention demonstrates cytostatic, antiinflammatory,  
 XX antineumatic, antiarthritic, antiasumatic, antiallergic, antibacterial,  
 XX antiviral, immunosuppressive, antidiabetic, neuroprotective, muscular and  
 XX dermatological activities and may be useful in gene therapy, ligand  
 XX binding assays or for diagnosing, preventing or treating a disease  
 XX selected from an inflammatory disease such as rheumatoid arthritis,  
 XX asthma or Crohn's disease, an allergic hypersensitivity, a bacterial or  
 XX viral infection, an autoimmune disorder such as type 1 diabetes, multiple  
 XX sclerosis, myasthenia gravis or systemic lupus erythematosus or cancer.  
 XX The current sequence is that of a single domain antibody (db)-related  
 XX light chain variable region E5sd protein of the invention.  
 XX  
 XX Sequence 108 AA:  
 XX  
 XX Query Match 82.3%; Score 489; DB 8; Length 108;  
 XX Best Local Similarity 85.7%; Pred. No. 2.4e-25;  
 XX Matches 96; Conservative 6; Mismatches 6; Indels 4; Gaps 1;  
 XX  
 XX QY 1 DIQMTGSPSSLSASVGVGVVITTCRASQSVSTSSYSYMHYQKKGKAPKVLISYASNLES 60  
 XX Db 1 DIQMTGSPSSLSASVGVGVVITTCRASQSVSTSSYSYMHYQKKGKAPKVLISYASNLES 60  
 XX 1 DIQMTGSPSSLSASVGVGVVITTCRASQSVSTSSYSYMHYQKKGKAPKVLISYASNLES 60  
 XX QY 61 GVPRFSGSGSGDTFTLTISLQPEDPATYTCQHSWGIPRTFGGTKEIKR 112  
 XX Db 57 GVPRFSGSGSGDTFTLTISLQPEDPATYTCQHSWGIPRTFGGTKEIKR 108  
 XX  
 XX RESULT 8  
 XX ID AAW90930 standard; protein; 238 AA.  
 XX  
 XX AAW90930;  
 XX  
 XX 08-AUG-2000 (first entry)  
 XX  
 XX Humanised anti-Fas designed light chain leu 1 protein.  
 XX  
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 XX anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;  
 XX dermatological; immunosuppressive; thymometric; antirheumatic; anti-Fas;  
 XX neurotrophic; antifertility; neuroprotective; antitumorogenic;  
 XX hepatotoxic; humanized; apocytosis; systemic lupus erythematosus;  
 XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 XX Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;

KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 XX Synthetic.  
 XX  
 XX EP90663-A2.  
 XX  
 XX 05-APR-2000.  
 XX  
 XX 29-SEP-1999; 99EP-00307711.  
 XX  
 XX 30-SEP-1998; 98JP-00276881.  
 XX 30-SEP-1998; 98JP-00276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI; 2000-258930/23.  
 XX N-PSDB; AAI1631.  
 XX  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 XX inflammatory or autoimmune disease, induces apoptosis selectively in  
 XX cells with abnormal Fas-Fas ligand systems.  
 XX  
 XX Claim 3; Page 156-157; 263pp; English.  
 XX  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 XX molecule (I) that induces apoptosis in cells with an abnormal Fas/Fas  
 XX ligand system, by binding to Fas on the cell surface, and prevents  
 XX apoptosis in cells with a normal system, by inhibiting binding between  
 XX Fas and its ligand. The products of the invention have anti-inflammatory,  
 XX anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
 XX immunomodulatory, dermatological, immunosuppressive, thymometric,  
 XX antineumatic, nephrotropic, antiferility, neuroprotective,  
 XX antiartherosclerotic, cardiac and hepatotropic activity. (I) induce  
 XX apoptosis by binding to cell surface Fas or inhibit it by competitive  
 XX inhibition of ligand binding. (I) are used to treat and/or prevent  
 XX diseases associated with the Fas/Fas ligand system, especially systemic  
 XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 XX versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 XX inhibit apoptosis in normal cells but selectively induce it in abnormal  
 XX cells. They bind to both human and murine Fas, so can be evaluated in  
 XX murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 XX the native ligand, do not induce liver disease, and have reduced risk of  
 XX inducing a human anti-murine antibody response. This sequence represents  
 XX a humanised anti-Fas antibody light chain construct designated leu 1  
 XX which is described in the method of the invention  
 XX  
 XX Sequence 238 AA:  
 XX  
 XX Query Match 82.3%; Score 489; DB 3; Length 238;  
 XX Best Local Similarity 86.0%; Pred. No. 4.7e-25;  
 XX Matches 96; Conservative 4; Mismatches 12; Indels 0; Gaps 0;  
 XX  
 XX QY 1 DIQMTGSPSSLSASVGVGVVITTCRASQSVSTSSYSYMHYQKKGKAPKVLISYASNLES 60  
 XX Db 21 DIQMTGSPSSLSASVGVGVVITTCRASQSVSTSSYSYMHYQKKGKAPKVLISYASNLES 60  
 XX QY 61 GVPRFSGSGSGDTFTLTISLQPEDPATYTCQHSWGIPRTFGGTKEIKR 114  
 XX Db 81 GVPRFSGSGSGDTFTLTISLQPEDPATYTCQHSWGIPRTFGGTKEIKR 134  
 XX  
 XX RESULT 9  
 XX ABB74899

ID ABB74899 standard; protein; 238 AA.  
 AC ABB74899;  
 XX  
 XX  
 DT 26-APR-2002 (first entry)  
 XX  
 XX Humanised anti-Fas antibody light chain SEQ ID NO 131.  
 DE  
 XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
 KM light chain subunit; apoptosis; immunosuppressive; antiallergic;  
 KM autoimmune disease; allergy; atopic.  
 OS Synthetic.  
 XX  
 PN JP2001342148-A.  
 XX  
 PD 11-DEC-2001.  
 XX  
 PF 28-MAR-2001; 2001JP-00093106.  
 XX  
 PR 29-MAR-2000; 2000JP-00090918.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 DR WPI; 2002-145113/19.  
 DR N-PSDB; ABL45939.  
 XX  
 PT Drug containing humanized anti-Fas antibody, used for preventing and  
 PT treating autoimmune diseases, allergy, and atopy.  
 XX  
 PS Claim 1; Page 133-134; 194pp; Japanese.  
 XX  
 CC The invention relates to a preventive or treating agent for diseases  
 CC caused by abnormality in Fas/Fas ligand system containing as the active  
 CC component an antibody having as the light chain subunit a polypeptide  
 CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
 CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
 CC fully defined in the specification and having an activity of combining  
 CC specifically with mammalian Fas and an activity of inducing apoptosis in  
 CC a cell expressing Fas. The agent has immunosuppressive and antiallergic  
 CC activity and is used for preventing and treating autoimmune diseases,  
 CC allergy, atopy and others  
 XX  
 SQ Sequence 238 AA;  
 QY Query Match 82.3%; Score 489; DB 5; Length 238;  
 Best Local Similarity 86.0%; Pred. No. 4.7e-25;  
 Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 DIQWTQSPSSLSASVGDRTVTTCRASQSVSTSSYSYMHYQOKRGKAPKVLISYASNLSS 60  
 DB 21 DIVLTQSPSSLSASVGDRTVTTCRASQSVYDGDSSYNNWYQOKRGKAPKLLIYAASNLSS 80  
 QY 61 GVPSRRSGSGSGDFTLTITSSLOPEDPATYCOHSGKIPRTGCGTVEIKRTV 114  
 DB 81 GVPSRRSGSGSGDFTLTITSSLOPEDPATYCOQSNEDPRTFGGTVEIKRTV 134  
 RESULT 10  
 AAM90932  
 ID AAM90932 standard; protein; 238 AA.  
 XX  
 AC AAM90932;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Humanised anti-Fas designed light chain Leu 3 protein.  
 XX  
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KM anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;  
 KM dermatological; immunosuppressive; chytromimetic; antirheumatic; anti-Fas;  
 KM nephrotropic; antiinfertility; neuroprotective; antiatherosclerotic;  
 KM hepatotropic; humanized; apoptosis; systemic lupus erythematosus;

KM Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KM Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KM Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KM multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KM cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 PN EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-00307711.  
 XX  
 PR 30-SEP-1998; 98JP-00276881.  
 PR 30-SEP-1998; 98JP-00276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haryuyama H, Nakahara K, Tamaki I, Takahashi T;  
 DR WPI; 2000-258930/23.  
 DR N-PSDB; AAAL1633.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems.  
 XX  
 PS Claim 3; Page 161-162; 263pp; English.  
 XX  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,  
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,  
 CC antiatherosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody light chain construct designated Leu 3  
 CC which is described in the method of the invention  
 XX  
 SQ Sequence 238 AA;  
 QY Query Match 82.2%; Score 488; DB 3; Length 238;  
 Best Local Similarity 85.1%; Pred. No. 5.4e-25;  
 Matches 97; Conservative 5; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 DIQWTQSPSSLSASVGDRTVTTCRASQSVSTSSYSYMHYQOKRGKAPKVLISYASNLSS 60  
 DB 21 DIVLTQSPSSLSASVGDRTVTTCRASQSVYDGDSSYNNWYQOKRGKAPKLLIYAASNLSS 80  
 QY 61 GVPSRRSGSGSGDFTLTITSSLOPEDPATYCOHSGKIPRTGCGTVEIKRTV 114  
 DB 81 GVPSRRSGSGSGDFTLTITSSLOPEDPATYCOQSNEDPRTFGGTVEIKRTV 134

RESULT 11
ID ABB74901 standard; protein: 238 AA.
XX ABB74901,
XX ABB74901;
DT 26-APR-2002 (first entry)
XX Humanised anti-Fas antibody light chain SEQ ID NO 52.
DE Humanised anti-Fas antibody light chain SEQ ID NO 52.
XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
XX autoimmune disease; allergy; atopic.
OS Synthetic.
PN JP2001342148-A.
XX JP2001342148-A.
PD 11-DEC-2001.
XX 11-DEC-2001.
PE 28-MAR-2001; 2001JP-00093106.
PR 29-MAR-2000; 2000JP-00090918.
PA (SANY ) SANKYO CO LTD.
DR WPI: 2002-145113/19.
DR N-PSDB; ABLL45941.
PT Drug containing humanized anti-Fas antibody, used for preventing and
XX treating autoimmune diseases, allergy, and atopy.
PS Example 14 (Preparatory); Page 94; 194pp; Japanese.
XX The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in Fas/Fas ligand system containing as the active
CC component an antibody having as the light chain subunit a polypeptide
CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
CC fully defined in the specification and having an activity of combining
CC specifically with mammalian Fas and an activity of inducing apoptosis in
CC a cell expressing Fas. The agent has immunosuppressive and antiallergic
CC activity and is used for preventing and treating autoimmune diseases,
CC allergy, atopy and others
SO Sequence 238 AA;
Query Match 82.2%; Score 488; DB 5; Length 238;
Best Local Similarity 85.1%; Pred. No. 5.4e-25;
Matches 97; Conservative 5; Mismatches 12; Indels 0; Gaps 0
OY 1 DIQNTGPPSSLSASVGDRTVTTCRASQSVSTSSYSTMTMYOQKPGAAFPVLISYSNIES 60
DB 21 DIVLTGSPSSLSASVGDRTVTTCRASQSYVDYDSDTMMYQOKPGAAPLTLIYASNDIES 80
OY 61 GVPSRFSGSSGGTDFTLTISIQLPDPATYYCOHSMGIQRFGQGKKVIKRTV 114
DB 81 GIPIRFSGSSGGTDFTLTISIQLPDPATYYCOQHSHEDRRITRGQTKVEIKRTV 134
RESULT 12
ID AAB45995 standard; peptide: 240 AA.
XX AAB45995,
AC AAB45995;
XX AAB45995;
DT 23-MAR-2001 (first entry)
XX 23-MAR-2001 (first entry)
DE Human MUC-1 scFv clone R2.
XX Human MUC-1 scFv clone R2.
MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
KW antidiabetic antibody; cytostatic; virucidal; antibacterial; TP antigen

KX		antiparasitic; infectious disease.
XX		
OS	Homo sapiens.	
PN	WO20073430-A2.	
PD	07-DEC-2000.	
XX		
PF	29-MAY-2000; 2000WO-DE001809.	
XX		
PR	27-MAY-1999; 99DE-01024405.	
PR	09-SEP-1999; 99DE-01043016.	
XX		
PA	(DEIB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX		
P1	Goletz S, Karsten U;	
DR	WPI, 2001-049937/06.	
XX		
PT	Vaccines against conformation-dependent or non-peptide antigens, based on	
PT	DNA encoding peptide which mimics the antigen, useful e.g. as antitumor	
XX	vaccines.	
PS		
XX	Disclosure; Page 5-9; 36pp; German.	
CC	This invention describes a novel vaccine (V1) against conformation-	
CC	dependent antigens (CDA) comprising DNA (I) and/or an antibody, or	
CC	peptide which immunologically imitates CDA, is new. (1) encodes a region	
CC	of an antiidiotypic antibody (Ab2) or another peptide which: (a)	
CC	specifically binds to the binding site of an antibody (Ab1) or an antigen	
CC	binding molecule; and (b) immunologically mimics the initial antigen. The	
CC	epitope is partially or completely conformation-dependent, and has an	
CC	immunogenic structure defined by a specific spatial conformation of amino	
CC	acids. (1) is used in the form of linear or circular naked DNA and/or	
CC	with a viral vector and/or adjuvants. The products of the invention have	
CC	cycotoxic, virucidal, antibacterial and antiparasitic. The invention	
CC	also describes (1) a corresponding vaccine (V2) against antigens which	
CC	are not proteins or peptides, as defined above but which have epitopes	
CC	which show an immunogenic structure; (2) preparing (V1) and (V2); (3)	
CC	human antiidiotypic antibody fragments against the MUC1-conformation	
CC	epitope having one of 31 approximately 60 residue amino acids sequences,	
CC	all fully defined in the specification; (4) MUC1-conformation epitope	
CC	mimics having one of 16 9-17 residue amino acid sequences, all fully in	
CC	the specification; (5) antiidiotypic antibody fragments against the TF	
CC	antigen having one of 24 approximately 200 residue amino acid sequences,	
CC	fully defined in the specification; (6) TF carbohydrate epitope mimetics	
CC	having one of 25 7-13 residue amino acid sequences, all fully defined in	
CC	the specification; and (7) DNA sequences encoding the fragments and	
CC	derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat	
CC	cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria	
CC	and parasites. The vaccines are effective in cases where vaccination has	
CC	previously not been possible	
XX		
SQ	Sequence 240 AA:	
QY	Query Match 82.2%; Score 488; DB 4; Length 240;	
Db	Best Local Similarity 85.7%; Pred. No. 5.5e-25;	
Matches	96; Conservative 6; Mismatches 6; Indels 4; Gaps 1	
QY	1 DIQNTQSSTLSASVGNRPVTITTCRASGVSTSSYSYMMHWYOOKPEKAKRVLISVANSNES 60	
Db	133 DIQMTQSSTLSASVGNRPVTITTCRASGSI-----SYLMWYOOKPEKAKRLITYHAFLOS 188	
QY	61 GVPSRFSGSGGGTFTLTITSLQPEDFATYYICQHSWGIPRTFGQGTKVEIKR 112	
Db	189 GVPSRFSGSGGGTFTLTITSLQPEDPFTYYICQHPMEPPRTIFGQTKVEIKR 240	
RESULT 13		
ID	AAM13922 standard; protein; 114 AA.	
AC	AAM13922;	

```

XX 15-MAY-1997 (first entry)
DT Light chain #1 for anti-HB virus antibody.
XX
DE
XX
XX Antibody; heavy chain; light chain; variable region; human; monoclonal;
KM complementarity determining region; human; adr type hepatitis B virus;
KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine.
XX
OS Homo sapiens.
XX
PN JF09020798-A.
XX
XX 21-JAN-1997.
PD
XX
XX 11-JUL-1995; 95JP-00174752.
PF
XX 11-JUL-1995; 95JP-00174752.
PR
XX 11-JUL-1995; 95JP-00174752.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
PA
XX WPI; 1997-140911/13.
DR N-PSDB; AAT60117.
XX
XX Human anti-Hepatitis B antibody - used in a adr type HB virus vaccine.
PT
XX Claim 7; Page 10-11; 20pp; Japanese.
XX
XX AAM13921-W13928 represent the sequences for the heavy and light chains of
CC the human monoclonal antibodies of the invention. The antibody of the
CC invention preferably contains the sequence represented by AAM13912 in the
CC complementarity determining region-1 (CDR-1) of the heavy chain variable
CC region. The antibody of the invention also contains the sequence
CC represented by AAM13913 in the CDR-3 of the light chain variable region.
CC The antibody is capable of binding to adr type hepatitis B (HB) virus
CC antigen. A human anti-HB virus monoclonal antibody preparation which is
CC highly safe and is effective to adr type HB virus can be provided, using
CC the monoclonal antibody. It can also be used as a vaccine against HB
CC infection.
XX
SQ Sequence 114 AA;
Query Match 81.8%; Score 486; DB 2; Length 114;
Best Local Similarity 84.1%; Pred. No. 4e-25;
Matches 95; Conservative 9; Mismatches 5; Indels 4; Gaps 1;
QY 2 IOMTQSSSLASVGDRTVITTCRASQSVSTSYSTMWYQOKRGAAPKVLISYASNLSSG 61
DB 1 LEMTQSSSLASVGDRTVITTCRASQSVSTSYSTMWYQOKRGAAPKVLISYASNLSSG 56
QY 62 VPSRFGSGSGGDTFTLTISLQPEDFATYTCQSHWGIPTFGQGTKEIKRTV 114
DB 57 VPSRFGSGSGGDTFTLTISLQPEDFATYTCQSHWGIPTFGQGTKEIKRTV 109
RESULT 14
AAM95654
ID AAM95654 standard; protein; 114 AA.
XX
AC AAM95654;
XX
XX 08-JUN-1999 (first entry)
DT
XX
XX Mus musculus anti-IgE e426 variable light chain.
DE
XX
XX Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
KM histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
XX eczema; anaphylactic shock; urticaria.
XX
OS Mus musculus.
XX
PN WO901556-A2.

```

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XX 14-JAN-1999.
PD
XX
XX 30-JUN-1998; 98MO-US013410.
PF
XX 02-JUL-1997; 97US-00887352.
PR
XX (GENTH ) GENENTECH INC.
PA
XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
PI
XX WPI; 1999-106057/09.
XX
XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerization and
PT substituting alternative residues and screening for affinity against the
PT target.
XX
XX Disclosure; Page 89-90; 129pp; English.
XX
XX The sequence is that of the variable light chain of e426. It was used as
CC part of a method to improve the affinity of anti-IgE antibodies such as
CC e26 and e27. The e26 and e27 antibodies can be used for reducing or
CC preventing IgE mediated production of histamine in a mammal. They can be
CC used for treating a disorder mediated by IgE such as hypersensitivity,
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
CC for affinity purification, detection and diagnosis
XX
SQ Sequence 114 AA;
Query Match 81.8%; Score 486; DB 2; Length 114;
Best Local Similarity 86.0%; Pred. No. 4e-25;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
QY 1 DIOMTQSSSLASVGDRTVITTCRASQSVSTSYSTMWYQOKRGAAPKVLISYASNLSS 60
DB 1 DIOMTQSSSLASVGDRTVITTCRASQSVSTSYSTMWYQOKRGAAPKVLISYASNLSS 60
QY 61 GVPSRFGSGSGGDTFTLTISLQPEDFATYTCQSHWGIPTFGQGTKEIKRTV 114
DB 61 GVPSRFGSGSGGDTFTLTISLQPEDFATYTCQSHWGIPTFGQGTKEIKRTV 114
RESULT 15
AAM95655
ID AAM95655 standard; protein; 114 AA.
XX
AC AAM95655;
XX
XX 08-JUN-1999 (first entry)
DT
XX
XX Mus musculus anti-IgE e25 variable light chain.
DE
XX
XX Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
KM histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
XX eczema; anaphylactic shock; urticaria.
XX
OS Mus musculus.
XX
PN WO901556-A2.
XX
XX 14-JAN-1999.
PD
XX
XX 30-JUN-1998; 98MO-US013410.
PF
XX 02-JUL-1997; 97US-00887352.
PR
XX (GENTH ) GENENTECH INC.
PA
XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
PI
XX
XX

```

DR WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by  
PT identifying aspartyl residues which undergo isomerisation and  
PT substituting alternative residues and screening for affinity against the  
PT target.

XX Disclosure; Page 90; 129pp; English.

XX The sequence is that of the variable light chain of e25. It was used as  
CC part of a method to improve the affinity of anti-IgE antibodies such as  
CC e26 and e27. The e26 and e27 antibodies can be used for reducing or  
CC preventing IgE mediated production of histamine in a mammal. They can be  
CC used for treating a disorder mediated by IgE such as hypersensitivity,  
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,  
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used  
CC for affinity purification, detection and diagnosis

XX Sequence 114 AA;

Query Match 81.8%; Score 486; DB 2; Length 114;  
Best Local Similarity 86.0%; Pred. No. 4e-25;  
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQWTQSPSLASVGRVTTTCRASQSVSTSSYSYMHYQOKPKAPKVLISYASNLDS 60  
Db 1 DIQWTQSPSLASVGRVTTTCRASQSVSTSSYSYMHYQOKPKAPKVLISYASNLDS 60  
QY 61 GVPFRFSGSGSGTDTFTLTISSLOPEDPATYVCOHSMGIPRTFGQGTKEIKRTV 114  
Db 61 GVPFRFSGSGSGTDTFTLTISSLOPEDPATYVCOHSMGIPRTFGQGTKEIKRTV 114

Search completed: December 29, 2004, 19:35:41  
Job time : 120.425 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 19:20:34 ; Search time 23.9742 Seconds  
(without alignments)  
457.521 Million cell updates/sec

Title: US-10-044-896-3

Perfect score: 594

Sequence: 1 DIQMTQSPSSSLASVGVDRVT.....SMGIPTFGGQTKVEIKRTV 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	81.3	123	2	IG kappa chain - h
2	482	81.1	127	2	IG kappa chain V-J
3	474	79.8	108	2	IG kappa chain V-r
4	473	79.6	122	2	IG kappa chain - h
5	462	77.8	108	1	IG kappa chain V-I
6	459	77.3	109	2	IG kappa chain - h
7	458	77.1	108	2	IG kappa chain V-r
8	457	76.9	131	2	IG kappa chain V-J
9	455	76.6	109	2	IG kappa chain - h
10	453	76.3	111	2	IG kappa chain V-J
11	451	75.9	129	2	IG kappa chain - h
12	451	75.9	108	2	IG kappa chain - h
13	448	75.4	125	2	IG kappa chain V-J
14	447.5	75.3	106	2	IG kappa chain - h
15	447	75.3	122	2	IG kappa chain - h
16	446	75.1	129	2	IG kappa chain V-r
17	444	74.7	117	2	IG kappa chain V-J
18	443	74.6	128	2	IG kappa chain V-r
19	442	74.4	108	2	IG kappa chain V-r
20	442	74.4	117	2	IG kappa chain V-J
21	442	74.4	120	2	IG kappa chain V-J
22	442	74.4	125	2	IG kappa chain - h
23	442	74.4	129	2	IG kappa chain V-r
24	441	74.2	107	2	IG kappa chain V
25	441	74.2	108	1	IG kappa chain V-I
26	440	74.1	108	1	IG kappa chain V-I
27	440	74.1	129	1	IG kappa chain pre
28	439.5	74.0	107	2	IG kappa chain V
29	439	73.9	132	2	IG kappa chain - h

30	438	73.7	108	1	IG kappa chain V-I
31	438	73.7	125	2	IG kappa chain - h
32	438	73.7	132	2	IG kappa chain V-r
33	437.5	73.7	125	2	IG kappa chain - h
34	437	73.6	108	1	IG kappa chain V-I
35	437	73.6	108	1	IG kappa chain V-I
36	437	73.6	108	2	IG kappa chain - h
37	437	73.6	125	2	IG kappa chain V-J
38	436	73.4	129	2	IG kappa chain V-r
39	435	73.2	111	1	IG kappa chain V-r
40	434	73.1	108	1	IG kappa chain V-r
41	434	73.1	109	2	IG kappa chain V-r
42	433	72.9	108	1	IG kappa chain V-I
43	433	72.9	126	2	IG kappa chain V-I
44	433	72.9	129	2	IG kappa chain - h
45	432.5	72.8	124	2	IG kappa chain V-J

## ALIGNMENTS

```
RESULT 1
S40331
IG kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S403312; MUID:94080891; PMID:8258341
A:Accession: S40331
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLB>
A:Cross-references: EMBL:X72441; NID:G443350; PIDN:CAAS1109.1; PID:G443351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:32-106/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 483; DB 2; Length 123;
Best Local Similarity 85.6%; Pred. No. 1.1e-32;
Matches 95; Conservative 7; Mismatches 5; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSSLASVGVDRVTTCRAQSQSVTSISYIMHWYQKAPKVLISASNTES 60
DB 17 DIQMTQSPSSSLASVGVDRVTTCRAQSIS-----SYLWYQKAPKVLISASNTES 72
QY 61 GVPKRFSGSGGTDFTLTISLSLOPEDPATYVCOHSMGIPTFGGQTKVEIK 111
DB 73 GVPKRFSGSGGTDFTLTISLSLOPEDPATYVCOQSYSTPTFGGQTKVEIK 123

RESULT 2
S40367
IG kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S403312; MUID:94080891; PMID:8258341
A:Accession: S40367
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLB>
A:Cross-references: EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 482; DB 2; Length 127;
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Db 1 ELVMTQSPSSLSASVGDVRVITTCRASQGIS---AYLWMYQOKPKAKPKVLISYASNLDS 56  
 Qy 61 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOHSMGIPRTFGQGTKEIKRT 113  
 Db 57 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOQSYSPRTFGQGTKEIKRT 109

## RESULT 7

S44122  
 Ig kappa chain V region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
 C/Accession: S44122  
 R/Hawkins, R.E.; Zhu, D.; Owecke, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
 Submitted to the EMBL Data Library, March 1994  
 A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
 A/Reference number: S44105  
 A/Accession: S44122  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-108 <HAM>  
 A/Cross-references: EMBL:Z31390; NID:9472976; PIDN:CAA83265.1; PID:9940533  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 458; DB 2; Length 108;  
 Best Local Similarity 82.1%; Pred. No. 1e-30;  
 Matches 92; Conservative 7; Mismatches 9; Indels 4; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDVRVITTCRASQSVSTSSSYMMWYQOKPKAKPKVLISYASNLDS 60  
 Db 1 DIQMTQSPSSLSASVGDVRVITTCRASQGIS---SYLWMYQOKPKAKPKVLISYASNLDS 56  
 Qy 61 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOHSMGIPRTFGQGTKEIKR 112  
 Db 57 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOQSYSPRTFGQGTKEIKR 108

## RESULT 8

S40352  
 Ig kappa chain V-J-C region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S40352  
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A/Title: Expressed human immunoglobulin chl genes and their hypermutation.  
 A/Reference number: S40312; MUID:94080891; PMID:8258341  
 A/Accession: S40352  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-131 <KLE>  
 A/Cross-references: EMBL:X72462; NID:9441392; PIDN:CAA51130.1; PID:9441393  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 457; DB 2; Length 131;  
 Best Local Similarity 79.8%; Pred. No. 1.5e-30;  
 Matches 91; Conservative 8; Mismatches 11; Indels 4; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDVRVITTCRASQSVSTSSSYMMWYQOKPKAKPKVLISYASNLDS 60  
 Db 21 DIQMTQSPSSLSASVGDVRVITTCRASQGIS---NYLWMYQOKPKAKPKVLISYASNLDS 76  
 Qy 61 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOHSMGIPRTFGQGTKEIKRTV 114  
 Db 77 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOQSYSPRTFGQGTKEIKRTV 130

## RESULT 9

S31981  
 Ig kappa chain - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C/Accession: S31981  
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations  
 A/Reference number: S31977  
 A/Accession: S31981  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-109 <POR>  
 A/Cross-references: EMBL:Z15077; NID:938493; PIDN:CAA78786.1; PID:938494  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 455; DB 2; Length 109;  
 Best Local Similarity 78.8%; Pred. No. 1.8e-30;  
 Matches 89; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDVRVITTCRASQSVSTSSSYMMWYQOKPKAKPKVLISYASNLDS 60  
 Db 1 ELVMTQSPSSLSASVGDVRVITTCRASQDIS---RYLWMYQOKPKAKPKVLISYASNLDS 56  
 Qy 61 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOHSMGIPRTFGQGTKEIKRT 113  
 Db 57 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOQSYSPRTFGQGTKEIKRT 109

## RESULT 10

S09963  
 Ig kappa chain V-J region (103-7E) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
 C/Accession: S09963  
 R/Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
 Eur. J. Immunol. 20, 771-777, 1990  
 A/Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibody.  
 A/Reference number: S09955; MUID:90269328; PMID:2347362  
 A/Accession: S09963  
 A/Molecule type: mRNA  
 A/Residues: 1-111 <REI>  
 A/Cross-references: UNIPROT:Q920B9; EMBL:X51851  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/16-94/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 453; DB 2; Length 111;  
 Best Local Similarity 74.8%; Pred. No. 2.7e-30;  
 Matches 83; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVRVITTCRASQSVSTSSSYMMWYQOKPKAKPKVLISYASNLDS 60  
 Db 1 DIVITQSPASLAVSLGRATISCRASQSVSSGSIYMMWYQOKPKAKPKVLISYASNLDS 60  
 Qy 61 GVPSRFSGSGSGTDFTLTITSSLPQPEDPATYVYCOHSMGIPRTFGQGTKEIKR 111  
 Db 61 GVPSRFSGSGSGTDFTLTINHPVEEDPATYVYCOHSMWEIPRTFGQGTKEIKR 111

## RESULT 11

S40317  
 Ig kappa chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S40317  
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A/Title: Expressed human immunoglobulin chl genes and their hypermutation.  
 A/Reference number: S40312; MUID:94080891; PMID:8258341  
 A/Accession: S40317



Mon Jan 3 13:22:47 2005

us-10-044-896-3.rpr

Page 5

Db 72 GVPNRFGSGSGTDFTLLISSLQPEDFGYYCQQTHTTPTFGQTKVEIK 122

Search completed: December 29, 2004, 19:36:34  
Job time : 24.9742 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 18:57:29 ; Search time 127.21 Seconds  
(without alignments)  
515.624 Million cell updates/sec

Title: US-10-044-896-3

Perfect score: 594

Sequence: 1 DIQWTQSPSSLSASVGRVT.....SMGIPTFGQGTKEIKRTV 114

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

1825181

Total number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	78.1	108	2 Q9UL77	P01607 homo sapien
2	462	77.8	108	2 Q9UL77	P01607 homo sapien
3	459	77.3	236	2 Q6GMX8	Q6GMX8 homo sapien
4	456.5	76.9	107	2 Q96SAS	Q96SAS homo sapien
5	455	76.6	236	2 Q6GMX0	Q6GMX0 homo sapien
6	454	76.4	236	2 Q6GMW1	Q6GMW1 homo sapien
7	444	74.7	236	2 Q6PIH7	Q6PIH7 homo sapien
8	444	74.7	236	2 AAH34141	AAH34141 homo sapi
9	441	74.2	108	1 KYLE_HUMAN	P01597 homo sapien
10	441	74.2	108	2 Q9UL70	P01606 homo sapien
11	440	74.1	108	1 KYLE_HUMAN	P01597 homo sapien
12	440	74.1	108	1 KYLE_HUMAN	P01597 homo sapien
13	440	74.1	236	2 Q7Z3V4	Q7Z3V4 homo sapien
14	438	73.7	108	1 KYLE_HUMAN	P01603 homo sapien
15	437	73.6	108	1 KYLE_HUMAN	P01594 homo sapien
16	437	73.6	108	1 KYLE_HUMAN	P01594 homo sapien
17	435	73.2	111	1 KYLE_HUMAN	P01670 mus musculu
18	434	73.1	108	1 KYLE_HUMAN	P01674 mus musculu
19	433	72.9	108	1 KYLE_HUMAN	P01599 homo sapien
20	431.5	72.6	107	2 Q9UL81	Q9UL81 homo sapien
21	431	72.6	236	2 Q6PIH5	Q6PIH5 homo sapien
22	431	72.6	236	2 AAH29444	AAH29444 homo sapi
23	429	72.2	108	1 KYLE_HUMAN	P01593 homo sapien
24	428	72.1	108	1 KYLE_HUMAN	P01607 homo sapien
25	428	72.1	111	2 Q920E9	Q920E9 mus musculu
26	428	72.1	234	2 Q7Z473	Q7Z473 homo sapien
27	427	71.9	111	1 KYLE_HUMAN	P01671 mus musculu
28	427	71.9	236	2 Q6GMX9	Q6GMX9 homo sapien
29	426	71.7	108	1 KYLE_HUMAN	P01608 homo sapien
30	426	71.7	108	1 KYLE_HUMAN	P01611 homo sapien
31	426	71.7	108	1 KYLE_HUMAN	P01612 homo sapien

32	425	71.5	108	1 KYLE_HUMAN	P01598 homo sapien
33	425	71.5	108	1 KYLE_HUMAN	P01605 homo sapien
34	425	71.5	108	2 Q9UL79	Q9UL79 homo sapien
35	422.5	71.1	109	1 KYLE_HUMAN	P01612 homo sapien
36	421.5	71.0	107	1 KYLE_HUMAN	P01595 homo sapien
37	421	70.9	108	1 KYLE_HUMAN	P01595 homo sapien
38	419	70.5	236	2 Q6PIH4	Q6PIH4 homo sapien
39	419	70.5	236	2 AAH34146	AAH34146 homo sapi
40	418	70.4	108	1 KYLE_HUMAN	P01610 homo sapien
41	417	70.2	111	1 KYLE_HUMAN	P01673 mus musculu
42	413	69.5	108	1 KYLE_HUMAN	P01604 homo sapien
43	413	69.5	111	1 KYLE_HUMAN	P01673 mus musculu
44	411	69.2	240	2 Q6PIH5	Q6PIH5 homo sapien
45	411	69.2	240	2 AAH17870	AAH17870 homo sapi

#### ALIGNMENTS

RESULT 1					
ID	Q9UL77	PRELIMINARY;	PRT;	108 AA.	
AC	Q9UL77;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9827139; PubMed=9614934;				
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,				
RA	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal				
RT	fecus."				
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL; AF035037; AAD56273.1; -.				
DR	PIR; B49047; B49047.				
DR	PIR; S34083; S34083.				
DR	HSP; P01607; 18MW.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; Ig_v. 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;				
Query Match 78.1%; Score 464; DB 2; Length 108;					
Best Local Similarity 82.1%; Pred. No. 1,7e-37;					
Matches 92; Conservative 8; Mismatches 8; Indels 4; Gaps 1;					
Qy	1	DIQWTQSPSSLSASVGRVTITTCRASQSVSTSSYSYMWYQKKGKAPKVLISYASNLES	60		
Db	1	DIQWTQSPSSLSASVGRVTITTCRASQSVSTSSYSYMWYQKKGKAPKVLISYASNLES	56		
Qy	61	GVPRFSGSGSGDTFTITISLQPEDPATYCCQHSKGIPTFGGTKEIKR	112		
Db	57	GVPRFSGSGSGDTFTITISLQPEDPATYCCQHSKGIPTFGGTKEIKR	108		
RESULT 2					
ID	KYLE_HUMAN	STANDARD;	PRT;	108 AA.	
AC	P01600;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-OCT-2004 (Rel. 45, Last annotation update)				

DE Ig kappa chain V-I region Hau.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
 chain of subgroup I (Bence-Jones Protein Hau): subdivision within  
 RT subgroups";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PIR: A01668; KIHUHU.  
 DR PDB: 1F6L; X-ray; L=1-108.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PS50835; Ig\_LIKE; 1.  
 KM 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 34 Complementarity-determining-1.  
 FT DOMAIN 35 49 Framework-2.  
 FT DOMAIN 50 56 Complementarity-determining-2.  
 FT DOMAIN 57 88 Framework-3.  
 FT DOMAIN 89 97 Framework-4.  
 FT DOMAIN 98 107 Complementarity-determining-3.  
 FT DISULFID 23 88 Framework-4.  
 FT NON\_TER 108 108 By similarity.  
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;  
 Query Match 77.8%; Score 462; DB 1; Length 108;  
 Best Local Similarity 82.1%; Pred. No. 2.7e-37;  
 Matches 92; Conservative 8; Mismatches 8; Indels 4; Gaps 1;  
 QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQSVSTSYSMYVQOKPKYLISYASNTLS 60  
 DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQSVSTSYSMYVQOKPKYLISYASNTLS 56  
 QY 61 GVPSRFGSGSGSDPTLTITSLQPEDPATYTCQHSWGIPTFGQGTVEIKR 112  
 DB 57 GVPSRFGSGSGSDPTLTITSLQPEDPATYTCQHSWGIPTFGQGTVEIKR 108  
 RESULT 3  
 ID Q6GKX8 PRELIMINARY; PRT; 236 AA.  
 AC Q6GKX8  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyanski M.I., Skalka U., Smalusz D.B., Schnerch A., Schein J.B.,  
 RA Jones S.J., Maizra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073764; AAH73764.1; -.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; C1-set; 1.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART: SM00409; Ig\_2.  
 DR SMART: SM00407; IgC1\_1.  
 DR SMART: SM00406; IgV\_1.  
 DR PROSITE: PS50835; Ig\_LIKE; 2.  
 DR PROSITE: PS02020; IG\_MHC; UNKNOWN\_1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;  
 Query Match 77.3%; Score 459; DB 2; Length 236;  
 Best Local Similarity 79.8%; Pred. No. 1.3e-36;  
 Matches 91; Conservative 9; Mismatches 10; Indels 4; Gaps 1;  
 QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQSVSTSYSMYVQOKPKYLISYASNTLS 60  
 DB 23 DIQMTQSPSSLSASVGDRTVITTCRASQSVSTSYSMYVQOKPKYLISYASNTLS 78  
 QY 61 GVPSRFGSGSGSDPTLTITSLQPEDPATYTCQHSWGIPTFGQGTVEIKR 114  
 DB 79 GVPSRFGSGSGSDPTLTITSLQPEDPATYTCQHSWGIPTFGQGTVEIKR 132  
 RESULT 4  
 ID Q96SA9 PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain  
 DE variable region (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.B., Shikhan A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin  
 RT antibody V region genes";  
 RL J. Immunol. 161:2020-2031 (1998).  
 DR EMBL; U96396; AAB68785.1; -.  
 DR PIR; B49047; B49047.  
 DR PIR; PH0867; PH0867.  
 DR PIR; S16840; S16840.



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DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSP; P01607; 1BWM.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT TER 107
SQ SEQUENCE 107 AA; 11520 MM; 4BB43B9C5B577F16 CRC64;

Query Match 76.9%; Score 456.5; DB 2; Length 107;
Best Local Similarity 83.0%; Pred. No. 9.1e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 5; Gaps 2;

Qy 1 DIQNTGSPSSLSASVGRVITTCRASQSVSTSSYSHMHWYQKPKAKPLIYASNSLS 60
Db 1 DIQNTGSPSSLSASVGRVITTCRASQSVSTSSYSHMHWYQKPKAKPLIYASNSLS 56
61 GVPSRFGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTFGQGTVEIKRTV 112
57 GVPSRFGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTFGQGTVEIKRTV 107

RESULT 5
ID O6GMX0 PRELIMINARY; PRT; 236 AA.
AC O6GMX0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisela K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skalela U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR InterPro; IPR003596; IG_v.
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DR Pfam; PF07654; Cl-sec; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MM; 864EA08C7B2BPAF CRC64;

Query Match 76.6%; Score 455; DB 2; Length 236;
Best Local Similarity 78.1%; Pred. No. 3.1e-36;
Matches 89; Conservative 12; Mismatches 9; Indels 4; Gaps 1;

Qy 1 DIQNTGSPSSLSASVGRVITTCRASQSVSTSSYSHMHWYQKPKAKPLIYASNSLS 60
Db 23 DIQNTGSPSSLSASVGRVITTCRASQSVSTSSYSHMHWYQKPKAKPLIYASNSLS 78
61 GVPSRFGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTFGQGTVEIKRTV 114
79 GVPSRFGSGSGDTFTLTISLQPEDPATYTCQHSWGIPTFGQGTVEIKRTV 112

RESULT 6
ID O6GMW1 PRELIMINARY; PRT; 236 AA.
AC O6GMW1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisela K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skalela U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
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DR	SMART; SM00407; IGC1; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SO	SEQUENCE 236 AA; 25751 MW; 5BPE6A087AFAC37 CRC64;
Query Match	
Best Local Similarity 76.4%; Score 454; DB 2; Length 236;	
Matches 91; Conservative 6; Mismatches 12; Indels 4; Gaps 1;	
QY	2 IOMTSPSLASVDRVTITCRASQSTSYSMHHYVQOKPGAPVLTISVAENISG 61
DB	24 IQMTSPSLASVDRVTITCRASQGSND---LGMVQKPGKAPLLIIYAASSLSG 79
QY	62 VPSRRSGSGCTDFLTITSLQPEFPATYYCOHSGMGRITRPGQGTKEVIEKTV 114
DB	80 VPSRRSGSGCTDFLTITSLQPEFPATYYCIQDYNVYWTGQGTKEVIEKTV 132

RESULT 7			
06PIH7			
ID	Q6PIH7	PRELIMINARY;	PRT; 236 AA.
AC	Q6PIH7/;		
DT	05-JUL-2004	(TRMBLrel. 27, Created)	
DT	05-JUL-2004	(TRMBLrel. 27, last sequence update)	
DT	05-JUL-2004	(TRMBLrel. 27, last annotation update)	
DE	Hypothetical protein.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxId:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RX	MEDLINE:22380257; PubMed:12477932;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Ditchenko L., Marninska K., Farmer A.A., Rudin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carrinot P., Prange C.,		
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahley J., Helton B., Kettelman W., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Schchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Kryzhanst M.I., Skalka U., Smalls D.E., Scherch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RA	Strauberg R.;		
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC034141; AAH34141.1; -		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG-cl.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF07654; Cl-set; 1.		
DR	Pfam; PFO0047; IG; 2.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGcl; 1.		
DR	SMART; SM00406; IGv; 1.		
DR	PROSITE; PSS00835; IG_LIKE; 2.		

DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;  
Query Match 74.7%; Score 44.1; DB 2; Length 236;  
Best Local Similarity 78.9%; Pred. NO. 3.7e-35;  
Matches 90; Conservative 6; Mismatches 14; Indels 4; Gaps 1.

[illegible]

ID	AAH34141	PRELIMINARY;	PR1;	236 AA.
AC	AAH34141;			
DT	02-MAR-2004 (TReMBLrel. 27, Created)			
DT	02-MAR-2004 (TReMBLrel. 27, last sequence update)			
DT	02-MAR-2004 (TReMBLrel. 27, last annotation update)			
OS	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RC	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,			
RA	Dickenson L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Bromstein M.J., Udell T.B., Toshitsuyuki S., Carninci P., Prange C.,			
RA	Raba S.A., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Rosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gnarinate P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whitely R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez M.C., Grimmud J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Kryzhanek M.I., Skalela U., Smalins D.E., Schnerch A., Schein J.E.,			
RA	Jones S.V., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	Strausberg R.;			
RA	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
RR	EMBL; BC034141; AAH34141.1; -.			
RW	Hypothetical protein.			
SQ	SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;			
Qy	Query Match 74.7%; Score 444; DB 2; Length 236;			
Qy	Best Local Similarity 78.9%; Pred. No. 3.7e-35;			
Qy	Matches 90; Conservative 6; Mismatches 14; Indels 4; Gaps 1;			
Db	1 DIQWTQSPSSILASVGDVVTITTCRASQSVSTSSYSYWHWTQOKRGKAPKVLISYASNIES 60			
Db	23 DIQWTQSPSSILASVGDVVTITTCRASQSVSTSSYSYWHWTQOKRGKAPKVLISYASNIES 78			
Qy	61 GVPRRFGSGSGSCDFTLITSSLOPEDPAATYCCQHSWICPRTFGGCTVEIKRTV 114			
Db	79 GVPRRFGSGSGSCDFTLITSSLOPEDPAATYCCQHSWICPRTFGGCTVEIKRTV 132			

```
RESULT 9
KVIE HUMAN STANDARD; PRT; 108 AA.
ID 015971
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
DR HSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6B350017F1E51 CRC64;

Query Match 74.2%; Score 441; DB 1; Length 108;
Best Local Similarity 77.7%; Pred. No. 3e-35;
Matches 87; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

Cy 1 DIQNTQSPSSLSASVGRVTITCRASQSVSTSSYSVMHWYQKQKAPKVLISYASNLIS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 BIZMTQSSSSLSASVGRVTITCRASQSVN---KILMWYQKQKAPKVLIPAASSLIS 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 61 GVPSRFSGSGGTFTLTISSLQPEDPATYCYQHSMGIPRTFGQGTVEIKR 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 GVPSRFSGSGGTFTLTISSLQPEDPATYCYCOGSYTPPYTFGQGTVEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID 09UL70;
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; Ig_I-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Query Match 74.2%; Score 441; DB 2; Length 108;
Best Local Similarity 79.5%; Pred. No. 3e-35;
Matches 89; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

Cy 1 DIQNTQSPSSLSASVGRVTITCRASQSVSTSSYSVMHWYQKQKAPKVLISYASNLIS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQNTQSPSSLSASVGRVTITCRASQGIS---NYLWYQKQKAPKVLISYASTLQS 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 61 GVPSRFSGSGGTFTLTISSLQPEDPATYCYQHSMGIPRTFGQGTVEIKR 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 GVPSRFSGSGGTFTLTISSLQPEDPATYCYQKNSAPRTFGQGTVEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
KVIN HUMAN STANDARD; PRT; 108 AA.
ID 01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
   chains.";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
   macroglobulin.
DR PIR; A01872; KIHUOU.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_I-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24A105827E CRC64;
```

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Query Match      74.1%; Score 440; DB 1; Length 108;
Best Local Similarity 69.6%; Pred. No. 3,7e-35;
Matches 78; Conservative 20; Mismatches 10; Indels 4; Gaps 1;

QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOQKRGKAPKYLISYASNL60
DB 1 DIQMTGSPSSLSASVGBRVITTCRASZTIS---SYLBMWZZXKRGKAPBLIYASBLHS 56

QY 61 GVPSPRFGSGSGGTDFTLTISLQPEDPATYTCQHSMGIPRTFGQTKVEIKR 112
DB 57 GVPSPRFGSGSGGTDFTLTISLQPEZPATYTCZSYSPPTFGGTRIZIKR 108

RESULT 12
KVLM HUMAN
ID_KVLM_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X00965; CA25477.1; ALT_TERM.
DR PIR; A01883; K1HWK.
DR HSSP; P01607; 1BWM.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 1 22
FT DOMAIN 23 129 Ig kappa chain V-I region Walker.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2P9 CRC64;

Query Match      74.1%; Score 440; DB 1; Length 129;
Best Local Similarity 79.3%; Pred. No. 4,6e-35;
Matches 88; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOQKRGKAPKYLISYASNL60
DB 23 DIQMTGSPSSLSASVGBRVITTCRASQIS---NYLWYQOQKRGKAPKYLISYASNL60 78

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QY 61 GVPSPRFGSGSGGTDFTLTISLQPEDPATYTCQHSMGIPRTFGQTKVEIKR 111
DB 79 GVPSPRFGSGSGGTDFTLTISLQPEZPATYTCZSYSPPTFGGTRIZIKR 129

RESULT 13
Q723Y4
ID Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal Muscle;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.B.,
RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC05332; AA05332.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR Hypothetical protein_236; UNKNOWN_1.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match      74.1%; Score 440; DB 2; Length 236;
Best Local Similarity 78.1%; Pred. No. 9,1e-35;
Matches 89; Conservative 8; Mismatches 13; Indels 4; Gaps 1;

QY 1 DIQMTGSPSSLSASVGDRTVITTCRASQSVSTSSYSYMHYQOQKRGKAPKYLISYASNL60
DB 23 DIQMTGSPSSLSASVGDRTVITTCRASQDIS---NYLWYQOQKRGKAPKYLISYASNL60 78
QY 61 GVPSPRFGSGSGGTDFTLTISLQPEDPATYTCQHSMGIPRTFGQTKVEIKR 114
DB 79 GVPSPRFGSGSGGTDFTLTISLQPEZPATYTCZSYSPPTFGGTRIZIKR 132

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RESULT 14
KV1K_HUMAN          STANDARD;          PRT;          108 AA.
ID   KV1K_HUMAN
AC   P01603
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region Ka.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_Taxid=9606;
RN   [1]
RP   MEDLINE=76189985; PubMed=818073;
RA   Shihoda T.;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1975).
CC   -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01869; KIHUKA.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig_V.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN          1      23      Framework-1.
FT   DOMAIN          24     34      Complementarity-determining-1.
FT   DOMAIN          35     49      Framework-2.
FT   DOMAIN          50     56      Complementarity-determining-2.
FT   DOMAIN          57     88      Framework-3.
FT   DOMAIN          89     97      Framework-4.
FT   DOMAIN          98    107      Complementarity-determining-3.
FT   DISULFID        23      88      Framework-4.
FT   NON_TER        108      By similarity.
SQ   SEQUENCE      108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match      73.7%; Score 438; DB 1; Length 108;
Best Local Similarity 73.2%; Pred. No. 5.9e-35;
Matches 82; Conservative 15; Mismatches 11; Indels 4; Gaps 1;

OY   1 DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHMYQOKPKAKPKVLISYASNL
DB   1 DIQMTQSPSTLSVSGDRVTITCRASQTV---LSYLMWYQOKPKAKPKVLISYASNL
OY   61 GVPSRFGSGSGSDFTLTITSSLOPEDPATYTCOHSMGIPRTFGGTVEIKR 112
DB   57 GVPSRFGSGSGGTBTFTTISVZPBFAITYCQZVLDPRTFGGTVEIKR 108

RESULT 15
KV1B_HUMAN          STANDARD;          PRT;          108 AA.
ID   KV1B_HUMAN
AC   P01594
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_Taxid=9606;
RN   [1]
RP   MEDLINE=72189444; PubMed=5028201;
RX   Schlecht H., Hillebrunn N.;
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"Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlgamer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigmann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the Bence-
RT   Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -1- MISCELLANEOUS: The structure of the V region was determined by
CC   molecular replacement methods using the known structure of the V
CC   region of the kappa chain RB1.
CC   -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PDB; 1JVS; X-ray; A=1-107.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig_V.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN          1      23      Framework-1.
FT   DOMAIN          24     34      Complementarity-determining-1.
FT   DOMAIN          35     49      Framework-2.
FT   DOMAIN          50     56      Complementarity-determining-2.
FT   DOMAIN          57     88      Framework-3.
FT   DOMAIN          89     97      Complementarity-determining-3.
FT   DISULFID        23      88      Framework-4.
FT   STRAND          4       5       By similarity.
FT   STRAND          10      13      1.
FT   STRAND          15      16      1.
FT   STRAND          19      25      1.
FT   STRAND          30      31      1.
FT   STRAND          33      38      1.
FT   STRAND          40      41      1.
FT   STRAND          44      49      1.
FT   STRAND          50      52      1.
FT   STRAND          53      54      1.
FT   TURN            56      57      1.
FT   TURN            60      61      1.
FT   STRAND          62      67      1.
FT   TURN            68      69      1.
FT   STRAND          70      75      1.
FT   STRAND          80      82      1.
FT   STRAND          85      90      1.
FT   STRAND          97      98      1.
FT   STRAND          102     106     1.
FT   NON_TER        108      108
SQ   SEQUENCE      108 AA; 11939 MW; E801187EE6F6B9 CRC64;

Query Match      73.6%; Score 437; DB 1; Length 108;
Best Local Similarity 78.6%; Pred. No. 7.3e-35;
Matches 88; Conservative 6; Mismatches 14; Indels 4; Gaps 1;

OY   1 DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHMYQOKPKAKPKVLISYASNL
DB   1 DIQMTQSPSSLSASVGDRVTITCRASQDIS---DYLMWYQOKPKAKPKVLISYASNL
OY   61 GVPSRFGSGSGSDFTLTITSSLOPEDPATYTCOHSMGIPRTFGGTVEIKR 112
DB   57 GVPSRFGSGSGAHTFTTISLOPEDPATYTCOOYDLPRTFGGTVEIKR 108
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Job time : 128.21 secs

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OM protein - protein search, using sw model

Run on: December 29, 2004, 19:36:01 ; Search time 93.9399 Seconds  
(without alignment)  
436.545 Million cell updates/sec

Title: US-10-044-896-3  
Perfect score: 594  
Sequence: 1 D10MTGSPSSLSASVGDVTVT.....SMGIPRTGQGTVEIKRTV 114

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1599051 seqs, 359727711 residues  
Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: Published Applications AA:\*
  - 2: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*
  - 3: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*
  - 4: /cgn2\_6/ptodata/2/pubppaa/US05\_PUBCOMB.pep:\*
  - 5: /cgn2\_6/ptodata/2/pubppaa/US04\_PUBCOMB.pep:\*
  - 6: /cgn2\_6/ptodata/2/pubppaa/US03\_PUBCOMB.pep:\*
  - 7: /cgn2\_6/ptodata/2/pubppaa/US02\_PUBCOMB.pep:\*
  - 8: /cgn2\_6/ptodata/2/pubppaa/US01\_PUBCOMB.pep:\*
  - 9: /cgn2\_6/ptodata/2/pubppaa/US00\_PUBCOMB.pep:\*
  - 10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*
  - 11: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*
  - 12: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*
  - 13: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*
  - 14: /cgn2\_6/ptodata/2/pubppaa/US05\_PUBCOMB.pep:\*
  - 15: /cgn2\_6/ptodata/2/pubppaa/US04\_PUBCOMB.pep:\*
  - 16: /cgn2\_6/ptodata/2/pubppaa/US03\_PUBCOMB.pep:\*
  - 17: /cgn2\_6/ptodata/2/pubppaa/US02\_PUBCOMB.pep:\*
  - 18: /cgn2\_6/ptodata/2/pubppaa/US01\_PUBCOMB.pep:\*
  - 19: /cgn2\_6/ptodata/2/pubppaa/US00\_PUBCOMB.pep:\*
  - 20: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	594	100.0	114	US-10-044-896-3	Sequence 3, Appl1
2	494	83.2	218	US-10-378-567-3	Sequence 3, Appl1
3	490	82.5	218	US-09-917-410-2	Sequence 2, Appl1
4	489	82.3	238	US-10-216-484-127	Sequence 127, App
5	489	82.3	238	US-10-384-933-127	Sequence 127, App
6	488	82.2	238	US-10-216-484-131	Sequence 131, App
7	488	82.2	238	US-10-384-933-131	Sequence 131, App
8	486	81.8	114	US-09-920-171-10	Sequence 10, Appl1
9	486	81.8	114	US-10-113-996-10	Sequence 10, Appl1
10	486	81.8	114	US-10-791-619-10	Sequence 9, Appl1
11	486	81.8	218	US-09-802-077-9	Sequence 9, Appl1
12	486	81.8	218	US-09-802-096-9	Sequence 9, Appl1
13	486	81.8	218	US-09-920-171-13	Sequence 13, Appl1

ALIGNMENTS

14	486	81.8	218	10	US-09-925-179-9	Sequence 9, Appl1
15	486	81.8	218	14	US-10-113-996-13	Sequence 13, Appl1
16	486	81.8	218	17	US-10-813-483-1	Sequence 1, Appl1
17	486	81.8	218	17	US-10-791-619-13	Sequence 13, Appl1
18	486	81.8	218	17	US-10-764-428-21	Sequence 21, Appl1
19	486	81.8	669	17	US-10-764-428-21	Sequence 21, Appl1
20	485	81.6	238	14	US-10-216-484-129	Sequence 129, App
21	485	81.6	238	14	US-10-384-933-129	Sequence 129, App
22	484	81.5	233	16	US-10-663-244-150	Sequence 150, App
23	483	81.3	108	17	US-10-409-814A-4	Sequence 4, Appl1
24	483	81.3	114	9	US-09-920-171-9	Sequence 9, Appl1
25	483	81.3	114	14	US-10-113-996-9	Sequence 9, Appl1
26	483	81.3	114	17	US-10-791-619-9	Sequence 9, Appl1
27	483	81.3	240	9	US-09-192-854-2	Sequence 2, Appl1
28	483	81.3	240	9	US-09-968-561A-2	Sequence 2, Appl1
29	483	81.3	240	10	US-09-968-744A-2	Sequence 2, Appl1
30	483	81.3	240	11	US-09-968-561A-2	Sequence 2, Appl1
31	483	81.3	240	17	US-10-744-774-1	Sequence 1, Appl1
32	482	81.1	108	17	US-10-744-774-17	Sequence 17, Appl1
33	481	81.0	111	9	US-09-920-171-7	Sequence 7, Appl1
34	481	81.0	111	14	US-10-113-996-7	Sequence 7, Appl1
35	481	81.0	111	17	US-10-791-619-7	Sequence 7, Appl1
36	480.5	80.9	110	9	US-09-025-403A-17	Sequence 17, Appl1
37	480.5	80.9	110	9	US-09-974-052-17	Sequence 17, Appl1
38	480.5	80.9	110	9	US-09-974-051-17	Sequence 17, Appl1
39	480.5	80.9	110	10	US-09-974-498-17	Sequence 17, Appl1
40	480.5	80.9	110	10	US-09-974-516-17	Sequence 17, Appl1
41	478	80.5	114	14	US-10-044-896-1	Sequence 1, Appl1
42	477.5	80.4	110	9	US-09-025-403A-15	Sequence 15, Appl1
43	477.5	80.4	110	9	US-09-974-052-15	Sequence 15, Appl1
44	477.5	80.4	110	9	US-09-974-051-15	Sequence 15, Appl1
45	477.5	80.4	110	10	US-09-974-498-15	Sequence 15, Appl1

RESULT 1  
US-10-044-896-3  
Sequence 3, Application US/10044896  
Publication No. US20030166228A1  
GENERAL INFORMATION:  
APPLICANT: Chantharapai, Anan  
APPLICANT: Kim, Jin K.  
APPLICANT: Stewart, Timothy  
TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES  
FILE REFERENCE: GENENT. 074A  
CURRENT APPLICATION NUMBER: US/10/044, 896  
CURRENT FILING DATE: 2002-01-09  
PRIOR APPLICATION NUMBER: 60/270775  
PRIOR FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: This sequence represents a humanized chimeric antibody comprising human and non-human sequences.  
US-10-044-896-3  
Query Match 100.0%; Score 594; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.8e-40;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 D10MTGSPSSLSASVGDVTVTTCRASQSVSTSSISYMWYQOXPGRKAPKLVISYASVLES 60  
DB 1 D10MTGSPSSLSASVGDVTVTTCRASQSVSTSSISYMWYQOXPGRKAPKLVISYASVLES 60  
QY 61 GVDSRFSGSGSGVDFTLTISLQPEDPATYCCQHSWGVIPTFGQGTVEIKRTV 114

Db 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114

## RESULT 2

US-10-378-567-3

/ Sequence 3, Application US/10378567  
/ Publication No. US20040006208A1  
/ GENERAL INFORMATION:  
/ APPLICANT: KARPUSAS, MICHAEL  
/ APPLICANT: HSU, YEN-MING  
/ APPLICANT: TAYLOR, FREDERICK R.  
/ APPLICANT: ZHENG, ZHONGLI  
/ TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 5C8 AND  
/ FILE REFERENCE: A096CON1  
/ CURRENT APPLICATION NUMBER: US/10/378,567  
/ PRIOR FILING DATE: 2003-02-28  
/ PRIOR APPLICATION NUMBER: PCT/US01/27352  
/ PRIOR FILING DATE: 2001-08-31  
/ PRIOR APPLICATION NUMBER: 60/276,452  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 60/229,933  
/ PRIOR FILING DATE: 2000-09-01  
/ NUMBER OF SEQ ID NOS: 3  
/ SOFTWARE: Patent Ver. 2.1  
/ SEQ ID NO 3  
/ LENGTH: 218  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: humanized 5c8 light chain amino acid  
US-10-378-567-3

Query Match 83.2%; Score 494; DB 15; Length 218;  
Best Local Similarity 79.8%; Pred. No. 3,7e-32;  
Matches 91; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNL 60

Db 1 DIVLTQSPATLSVSPERATISCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNL 60

QY 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114  
Db 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114

## RESULT 3

US-09-917-410-2

/ Sequence 2, Application US/09917410  
/ Patent No. US20020098183A1  
/ GENERAL INFORMATION:  
/ APPLICANT: MARTIN, Ulrich; HASLBECK, Anton; SCHUMACHER, Guenther;  
/ APPLICANT: CO, Man S.  
/ TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF  
/ MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR  
/ PREVENTION OF ACUTE ORGAN DAMAGE AFTER  
/ EXTRACORPOREAL BLOOD CIRCULATION  
/ NUMBER OF SEQUENCES: 6  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Felte & Lynch  
/ STREET: 805 Third Avenue  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: U.S.A.  
/ ZIP: 10022  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" Computer Disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: ASCII, Wordperfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/917,410

/ FILING DATE: 26-Jul-2001  
/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 08/578,953

/ FILING DATE: <Unknown>

/ APPLICATION NUMBER: EP 95 114 969.9

/ FILING DATE: 19-Sep-95

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Hanson, NO. US20020098183A1man D.

/ REGISTRATION NUMBER: 30,946

/ REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (212) 688-9200

/ TELEFAX: (212) 838-3884

/ INFORMATION FOR SEQ ID NO: 2:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 218

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 82.5%; Score 490; DB 9; Length 218;  
Best Local Similarity 86.0%; Pred. No. 7.8e-32;  
Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNL 60

Db 1 DIVLTQSPATLSVSPERATISCRASQSVSYDGDSTYMHYQOKPGKAPKVLISYASNL 60

QY 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114  
Db 61 GVPSPSGSGSGTDFLTITSSLOPEDFATYYCOHSGWIGIPRTFGQGTKEIKRTV 114

## RESULT 4

US-10-216-484-127

/ Sequence 127, Application US/10216484  
/ Publication No. US20030103976A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Setizawa, NO. US20030103976A1ufusa  
/ APPLICANT: Haruyama, Hideyuki  
/ APPLICANT: Nakahara, Kaori  
/ APPLICANT: Tamaki, Ikuro  
/ APPLICANT: Takahashi, Toku  
/ TITLE OF INVENTION: Anti-Fas Antibodies  
/ FILE REFERENCE: 980126CIP/HG  
/ CURRENT APPLICATION NUMBER: US/10/216,484  
/ CURRENT FILING DATE: 2002-08-09  
/ PRIOR APPLICATION NUMBER: US/09/499,662  
/ PRIOR FILING DATE: 2000-02-09  
/ PRIOR APPLICATION NUMBER: US 09/053,583  
/ PRIOR FILING DATE: 1998-04-01  
/ NUMBER OF SEQ ID NOS: 165  
/ SEQ ID NO 127  
/ LENGTH: 238  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Designed light  
/ OTHER INFORMATION: chain of humanized anti-Fas antibody  
US-10-216-484-127

Query Match 82.3%; Score 489; DB 14; Length 238;  
Best Local Similarity 86.0%; Pred. No. 1e-31;  
Matches 98; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTITTCRASQSVSTSSYSYMHYQOKPGKAPKVLISYASNL 60  
Db 21 DIVLTQSPATLSASVGDRTITTCRASQSVSYDGDSTYMHYQOKPGKAPKVLISYASNL 80



**Oy**      61 GVSRRFGSSSGDTFTLTISLQEDPATYTCQHSWGLPRTFGGKVKELKRTV 114  
         |||||  
**Db**      81 GVSRRFGSSSGDTFTLTISLQEDPATYTCQGSNEDPRTFGGKVKELKRTV 134

RESULT 5  
 US-10-384-933-127  
 Sequence 127, Application US/10384933  
 Publication No. US20030170817A1  
 GENERAL INFORMATION:  
 APPLICANT: Serizawa, No. US20030170817A1ufusa  
 APPLICANT: Haruyama, Hideyuki  
 APPLICANT: Nakahara, Kaori  
 APPLICANT: Tamaki, Ikuko  
 APPLICANT: Takahashi, Toru  
 TITLE OF INVENTION: Anti-Fas Antibodies  
 FILE REFERENCE: 980126C1P/HG  
 CURRENT APPLICATION NUMBER: US/10/384,933  
 CURRENT FILING DATE: 2003-02-05  
 PRIOR APPLICATION NUMBER: US/09/499,662  
 PRIOR FILING DATE: 2000-02-09  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583  
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01  
 NUMBER OF SEQ ID NOS: 165  
 SEQ ID NO 127  
 LENGTH: 238  
 TYPE: PR1  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Designed light  
 OTHER INFORMATION: chain of humanized anti-Fas antibody  
 US-10-384-933-127

RESULT 6  
US-10-216-484-131  
Sequence 131, Application US/10216484  
Publication No. US20030103976A1  
GENERAL INFORMATION:  
APPLICANT: Serizawa, No. US20030103976A1ufusa  
APPLICANT: Haruyama, Hideyuki  
APPLICANT: Nakahara, Kaori  
APPLICANT: Tamaki, Yuko  
APPLICANT: Takahashi, Toru  
TITLE OF INVENTION: Anti-Fas Antibodies  
FILE REFERENCE: 980126CIP/HG  
CURRENT APPLICATION NUMBER: US/10/216, 484  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US/09/499, 662  
PRIOR FILING DATE: 2000-02-09  
PRIOR APPLICATION NUMBER: US 09/053, 583  
PRIOR FILING DATE: 1998-04-01  
NUMBER OF SEQ ID NOS: 165  
SEQ ID NO 131  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Designed light  
US-10-216-484-131  
OTHER INFORMATION: chain of humanized anti-Fas antibody

Query Match	82.2%	Score 488	DB 14	Length 238
Best Local Similarity	85.1%	Pred. No. 1.2e-31		
Matches 97	Conservative	5	Mismatches 12	Indels 0
				Gaps 0

```

RESULT 7
US-10-384-933-131
/ Sequence 131, Application US/10384933
/ Publication No. US20030170817A1
/ GENERAL INFORMATION:
/ APPLICANT: Serizawa, No. US20030170817A1ufusa
/ APPLICANT: Haruyama, Hideyuki
/ APPLICANT: Nakahara, Kaori
/ APPLICANT: Tamaki, Ikuko
/ APPLICANT: Takahashi, Tokuo
/ TITLE OF INVENTION: Anti-Fas Antibodies
/ FILE REFERENCE: 980126CIP/HG
/ CURRENT APPLICATION NUMBER: US/10/384,933
/ CURRENT FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: US/09/499,662
/ PRIOR FILING DATE: 2000-02-09
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
/ NUMBER OF SEQ ID NOS: 165
/ SEQ ID NO 131
/ LENGTH: 238
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Designed light
/ OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-131

Query Match      82.2%; Score 488; DB 14; Length 238;
Best Local Similarity 85.1%; Pred. No. 1,2e-31;
Matches 97; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Cy      1 DQMTQSPSSLSASVGDRVTITCRASQSVSTSSYNMHWYQKQKPKVLISYASINLES 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      21 DIVLTQSPSSLSASVGDRVTITCRASQSVDPDGSYNMHWYQKQKPKVLISYASINLES 80

Cy      61 GVERPFGSGSGDTFTLTISLQPEDPATYYCQMSKGIPIRFGGGTAYEIRRTV 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      81 GIPSRFGSGSGDTFTLTISLQPEDPATYYCQMSKEDPRTGGGTAYEIRRTV 134

RESULT 8
US-09-920-171-10
/ Sequence 10, Application US/09920171
/ Patent No. US20020054878A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardiou, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
/ FILE REFERENCE: P1123C2US
/ CURRENT APPLICATION NUMBER: US/09/920,171
/ CURRENT FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: US 06/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 44

```

```
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-10
```

```
Query Match      81.8%; Score 486; DB 9; Length 114;
Best Local Similarity 86.0%; Pred. No. 8.8e-32;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVDGVITTCRASQSYSTSYMHWYQKPKGAPKYLISYASNLSS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVDGVITTCRASQSYVDYDGDSTMNWYQKPKGAPKLLIYAASYLE 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 GVPSPRSGSGSGTDFLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 9
US-10-113-996-10
/ Sequence 10, Application US/10113996
/ Publication No. US2003014924A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-IGB Antibodies
/ FILE REFERENCE: P1123C3US
/ CURRENT APPLICATION NUMBER: US/10/113,996
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: US 09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-10
```

```
Query Match      81.8%; Score 486; DB 14; Length 114;
Best Local Similarity 86.0%; Pred. No. 8.8e-32;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVDGVITTCRASQSYSTSYMHWYQKPKGAPKYLISYASNLSS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVDGVITTCRASQSYVDYDGDSTMNWYQKPKGAPKLLIYAASYLE 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 GVPSPRSGSGSGTDFLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 GVPSPRSGSGSGTDFLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 10
US-10-791-619-10
/ Sequence 10, Application US/10791619
/ Publication No. US2004029077A1
/ GENERAL INFORMATION:
/ APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
/ TITLE OF INVENTION: Improved Anti-IGG Antibodies and Method of Improving Polypeptides
/ FILE REFERENCE: P1123R1
/ CURRENT APPLICATION NUMBER: US/10/791,619
/ CURRENT FILING DATE: 2004-03-02
/ PRIOR APPLICATION NUMBER: US/09/109,207
```

```
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/051,554
/ PRIOR FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 10
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: Artificial
/ LOCATION: 1-114
/ OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-791-619-10
```

```
Query Match      81.8%; Score 486; DB 17; Length 114;
Best Local Similarity 86.0%; Pred. No. 8.8e-32;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVDGVITTCRASQSYSTSYMHWYQKPKGAPKYLISYASNLSS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVDGVITTCRASQSYVDYDGDSTMNWYQKPKGAPKLLIYAASYLE 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 GVPSPRSGSGSGTDFLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 11
US-09-802-077-9
/ Sequence 9, Application US/09802077
/ Patent No. US2001003842A1
/ GENERAL INFORMATION:
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
/ FILE REFERENCE: P0718P2C2US
/ CURRENT APPLICATION NUMBER: US/09/802,077
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 08/405,617
/ PRIOR FILING DATE: 1995-03-15
/ PRIOR APPLICATION NUMBER: US 08/185,899
/ PRIOR FILING DATE: 1994-01-26
/ PRIOR APPLICATION NUMBER: PCT/US92/06860
/ PRIOR FILING DATE: 1992-08-14
/ PRIOR APPLICATION NUMBER: US 07/879,495
/ PRIOR FILING DATE: 1992-05-07
/ PRIOR APPLICATION NUMBER: US 07/744,768
/ PRIOR FILING DATE: 1991-08-14
/ NUMBER OF SEQ ID NOS: 64
/ SEQ ID NO 9
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: humanized mae11, version 1, light chain
US-09-802-077-9
```

```
Query Match      81.8%; Score 486; DB 9; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVDGVITTCRASQSYSTSYMHWYQKPKGAPKYLISYASNLSS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLSASVDGVITTCRASQSYVDYDGDSTMNWYQKPKGAPKLLIYAASYLE 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 GVPSPRSGSGSGTDFLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 GVPSPRSGSGSGTDFLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 12
US-09-802-096-9
/ Sequence 9, Application US/09802096
```

```
/ Patent No. US20010038839A1
/ GENERAL INFORMATION:
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
/ FILE REFERENCE: P0718P2C3US
/ CURRENT APPLICATION NUMBER: US/09/802,096
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 08/405,617
/ PRIOR FILING DATE: 1995-03-15
/ PRIOR APPLICATION NUMBER: US 08/185,899
/ PRIOR FILING DATE: 1994-01-26
/ PRIOR APPLICATION NUMBER: PCT/US92/06860
/ PRIOR FILING DATE: 1992-08-14
/ PRIOR APPLICATION NUMBER: US 07/879,495
/ PRIOR FILING DATE: 1992-05-07
/ PRIOR APPLICATION NUMBER: US 07/744,768
/ PRIOR FILING DATE: 1991-08-14
/ NUMBER OF SEQ ID NOS: 64
/ SEQ ID NO 9
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: humanized mael1, version 1, light chain
US-09-802-096-9

Query Match      81.8%; Score 486; DB 9; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Cy 1 DIGNTQSPSSLSASVGRVITTCRASQSVSTSSYSYHMYQOKRGKAPKVLISYASNL 60
Db 1 DIGNTQSPSSLSASVGRVITTCRASQSVSDYDGSYHMYQOKRGKAPKVLISYASNL 60
61 GVPSRFSGSGSGDTFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 114
61 GVPSRFSGSGSGDTFTLTISLSLOPEDPATYTCQSHEDPTFGGTVEIKRTV 114

RESULT 13
US-09-920-171-13
/ Sequence 13, Application US/09920171
/ Patent No. US20020054878A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-1gE Antibodies (as amended)
/ FILE REFERENCE: P1123C2US
/ CURRENT APPLICATION NUMBER: US/09/920,171
/ CURRENT FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 13
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: light chain sequence derived from MAB11
US-09-920-171-13

Query Match      81.8%; Score 486; DB 9; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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Cy 1 DIGNTQSPSSLSASVGRVITTCRASQSVSTSSYSYHMYQOKRGKAPKVLISYASNL 60
Db 1 DIGNTQSPSSLSASVGRVITTCRASQSVSDYDGSYHMYQOKRGKAPKVLISYASNL 60
61 GVPSRFSGSGSGDTFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 114
61 GVPSRFSGSGSGDTFTLTISLSLOPEDPATYTCQSHEDPTFGGTVEIKRTV 114

RESULT 14
US-09-925-179-9
/ Sequence 9, Application US/09925179
/ Publication No. US20030044858A1
/ GENERAL INFORMATION:
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Anti-1gE Antibodies (as amended)
/ FILE REFERENCE: P0718P2C1C1US
/ CURRENT APPLICATION NUMBER: US/09/925,179
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 08/466,163
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: US 08/405,617
/ PRIOR FILING DATE: 1995-03-15
/ PRIOR APPLICATION NUMBER: US 08/185,899
/ PRIOR FILING DATE: 1994-01-26
/ PRIOR APPLICATION NUMBER: PCT/US92/06860
/ PRIOR FILING DATE: 1992-08-14
/ PRIOR APPLICATION NUMBER: US 07/879,495
/ PRIOR FILING DATE: 1992-05-07
/ PRIOR APPLICATION NUMBER: US 07/744,768
/ PRIOR FILING DATE: 1991-08-14
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 9
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: humanized mael1, version 1, light chain
US-09-925-179-9

Query Match      81.8%; Score 486; DB 10; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Cy 1 DIGNTQSPSSLSASVGRVITTCRASQSVSTSSYSYHMYQOKRGKAPKVLISYASNL 60
Db 1 DIGNTQSPSSLSASVGRVITTCRASQSVSDYDGSYHMYQOKRGKAPKVLISYASNL 60
61 GVPSRFSGSGSGDTFTLTISLSLOPEDPATYTCQHSWGIPTFGGTVEIKRTV 114
61 GVPSRFSGSGSGDTFTLTISLSLOPEDPATYTCQSHEDPTFGGTVEIKRTV 114

RESULT 15
US-10-113-996-13
/ Sequence 13, Application US/10113996
/ Publication No. US20030149244A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowman, Henry B.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Lowe, John
/ TITLE OF INVENTION: Improved Anti-1gE Antibodies
/ FILE REFERENCE: P1123C3US
/ CURRENT APPLICATION NUMBER: US/10/113,996
/ CURRENT FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: US 08/887,352
/ PRIOR FILING DATE: 1997-07-02
/ PRIOR APPLICATION NUMBER: US 09/296,005
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: US 09/920,171
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 13
/ LENGTH: 218
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-13
```

```
Query Match      81.8%; Score 486; DB 14; Length 218;
Best Local Similarity 86.0%; Pred. No. 1.6e-31;
Matches 98; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
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QY 1 DIQMTQSPSSLSASVDGRVTITCRASQSVSTSSYSMMHWYQKPKGKAPKVLISYASNTLS 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVDGRVTITCRASQSVSTSSYSMMHWYQKPKGKAPKVLISYASNTLS 60
```

```
QY 61 GVPSPRFGSGSGGTDFTLTITSLQPEDPATYVCOHSGIGIPRTFGQGTKEIKRTV 114
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GVPSPRFGSGSGGTDFTLTITSLQPEDPATYVCOHSGIGIPRTFGQGTKEIKRTV 114
```

```
Search completed: December 29, 2004, 19:52:39
Job time : 94.9399 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 18:57:29 ; Search time 132.79 Seconds  
(without alignments)  
515.624 Million cell updates/sec

Title: US-10-044-896-5

Perfect score: 634  
Sequence: 1 EVGLVESGGGVGPGRGSLRL.....ISDFPDWGGQTLVTVSAS 119

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	447	70.5	470	2	Q6PJ44
2	447	70.5	470	2	AAH18747
3	433.5	68.4	121	2	BAD00525
4	428	67.5	113	2	Q9UL90
5	428	67.5	120	2	BAD00414
6	427.5	67.4	473	2	Q6MZV7
7	427.5	67.4	473	2	CAE45920
8	427	67.4	128	2	BAD00406
9	427	67.4	128	2	BAD00444
10	426	67.2	121	2	Q9UL71
11	426	67.2	122	2	BAD00446
12	425.5	67.1	123	2	BAD00520
13	425.5	67.1	479	2	AAH06402
14	424.5	67.0	613	2	Q6WUX1
15	424	66.9	120	2	BAD00531
16	424	66.9	493	2	Q6GMX2
17	423.5	66.8	119	2	BAD00556
18	423.5	66.8	471	2	AAH24289
19	420.5	66.3	131	2	BAD00433
20	420	66.2	120	2	BAD00465
21	419.5	66.2	483	2	Q6MZ99
22	419.5	66.2	483	2	CAE45898
23	418.5	66.0	121	2	BAD00463
24	418.5	66.0	125	2	BAD00439
25	418	65.9	120	2	BAD00507
26	418	65.9	597	2	Q96BB9
27	416.5	65.7	121	2	BAD00404
28	416.5	65.7	606	2	Q6GM72
29	416	65.6	120	2	BAD00488
30	416	65.6	126	2	BAD00529
31	416	65.6	464	2	Q6MZU6

32	416	65.6	464	2	CAE45931	CAE45931 homo sapi
33	415.5	65.5	125	2	BAD00448	BAD00448 camelus d
34	415.5	65.5	127	2	BAD00564	BAD00564 camelus d
35	415.5	65.5	465	2	Q6P6C4	Q6P6C4 homo sapien
36	415.5	65.5	465	2	AAH62335	AAH62335 homo sapi
37	415	65.5	116	2	Q9UL93	Q9UL93 homo sapien
38	415	65.5	122	2	BAD00470	BAD00470 camelus d
39	414.5	65.4	119	2	BAD00471	BAD00471 camelus d
40	414	65.3	117	2	AAH35875	AAH35875 lama glam
41	414	65.3	118	2	BAD00487	BAD00487 camelus d
42	414	65.3	120	2	BAD00493	BAD00493 camelus d
43	414	65.3	120	2	BAD00503	BAD00503 camelus d
44	414	65.3	120	2	BAD00544	BAD00544 camelus d
45	414	65.3	126	2	BAD00566	BAD00566 camelus d

## ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	470 AA.
ID Q6PJ44			
AC Q6PJ44			
DT 05-JUL-2004 (TREMBLrel. 27, Created)			
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE Hypothetical protein.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX NCBI_Taxid=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Primary B-Cells;			
RX MEDLINE=22388257; PubMed=12477932;			
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.B., Scheetz T.E.,			
RA Brownstein M.J., Uediri T.B., Toshiyuki S., Carninci P., Prange C.,			
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huily S.W.,			
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA Fahey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,			
RA Whitkey R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,			
RA Krzywinski M.I., Skelton U., Smalton D.B., Scherch A., Schein J.E.,			
RA Jones S.J., Marra M.A.,			
RT "Generation and initial analysis of more than 15,000 full-length human			
RT and mouse cDNA sequences";			
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Primary B-Cells;			
RA Strausberg R.,			
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR EMBL: BC018747; AAH18747.1; -			
DR InterPro: IPR003599; IG_1like.			
DR InterPro: IPR007110; IG_1like.			
DR InterPro: IPR003597; IG_c1.			
DR InterPro: IPR003006; IG_MHC.			
DR InterPro: IPR003596; IG_v.			
DR Pfam: PF00654; C1-sect; 3.			
DR Pfam: PF00647; Ig; 4.			
DR SMART: SM00409; Ig; 2.			
DR SMART: SM00407; Igcl; 3.			
DR SMART: SM00406; IGV; 1.			
DR PROSITE: PS00835; IG_LIKE; 4.			
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.			

KW	Hypothetical protein.
5Q	SEQUENCE 470 AA, 51715 MW, 7849556A11FDD99 CXC64;
	Query Match 70.5%; Score 447; DB 2; Length 470;
	Best Local Similarity 72.4%; Pred. No. 8,3e-39;
	Matches 89; Conservative 7; Mismatches 23; Indels 4; Gaps 1;
QY	1 EVVLVESGGGLVQPGSGLRLLSCATSGYFTETXIIHNVQARQKGLIEWVASINPDYDINTY 60
DB	20 EVOLVESGGGLVQPGSGLRLLSCVVSGLPTSSWMSWVQAQPKGLEVAANTIKODSEKKY 79
QY	61 NORFGRFTTSLDSKRTAVLQOMNSLRADPAVYYCA----SWISDFPDYWGQGLTVLTVS 116
DB	80 VDSVYGRFTTISRDNAKNSLYIQMNSLRADPAVYYCAADSGSWYRWDMDPNGGGLTVLVS 139
QY	117 SAS 119
DB	140 SAS 142

RESULT 2	ID	AAH18747	PRELIMINARY;	PRT;	470 AA.
AC	AAH18747;				
DT	02-MAR-2004	(TREMBLrel. 27, Created)			
DT	02-MAR-2004	(TREMBLrel. 27, Last sequence update)			
DT	02-MAR-2004	(TREMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
NP					
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Gronow L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shemem C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Bueckow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Dickenson L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stepleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udell T.B., Toshfayuk S., Carinini P., Prange C.,				
RA	Rana S.S., Loguanello N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Falley J., Helton E., Ketteman W., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Kryzhanovskii M.I., Skalka U., Smalins D.E., Scherch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RA	Strausberg R.;				
RA	Submitted (DEC-2001) to the EMBL/Genbank/DBSJ databases.				
DR	EMBL, BC018747, AAH18747.1; -.				
DR	Hypothetical protein.				
SO	SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;				

Query Match	70.5%;	Score 447;	DB 3;	Length 470;
Best Local Similarity	72.4%;	Pred. No. 8.3e-39;		
Matches 89; Conservative	7;	Mismatches 23;	Indels 4;	Gaps 1;

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Oy      1 EVQLVESGGGLVQPGGSLRLSCATSGYFTETYYIMHWROAPGKGLEWVASINPDYDITNY 60
        |||||
Db    20 EVQLVESGGGLVQPGGSLRLSCAVSGFTSSYMMSWVRQAPGKGLEWVANIKQDGSEKYI 79
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QY      61  NQRFGRGRTISLDKSRFAYLQMSLRADDTAVYCA-----SWISPFYMGQGLVTAS 116
      80  VDSVGRGRTISLDKSNKNSLYLQMSLRADDTAVYCARQSSWYRWPFQMGQGLVTAS 139
Db
QY      117 SAS 119
      140 SAS 142
Db
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RESULT 3			
BAD00525			
ID	BAD00525	PRELIMINARY;	PR; 121 AA.
AC	BAD00525;		
DT	02-MAR-2004 (TrEMBLrel. 27, Created)		
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)		
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Immunoglobulin heavy chain VHJF region (Fragment).		
CN	IGH.		
OS	Camelus dromedarius (Dromedary) (Arabian camel).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus		
OX	NCBI_TaxID=9838;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Spleen;		
RA	Honda T., Akahori Y., Kurosawa Y.;		
RT	"Libraries of heavy-chain antibodies reflecting camel gamma2 and		
RT	gamma3 in vivo repertoirees.";		
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB092163; BAD00525.1; -.		
FT	NON_TER	1	
FT	NON_TER	121	
SQ	SEQUENCE	121 AA; 12951 MW; A6D50E79D505E5B4 CRC64;	

Query Match	68.4%	Score 433.5	DB 2	Length 121
Best Local Similarity	71.1%	Pred No. 4.7e-38		
Matches	86	Conservative	9	Mismatches 23
				Indels 3
				Gaps 2
QY	1	EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYIMHWRAQPGKGLEWVASINDYDITNY	60	
Db	1	DYQLVESGGGLVQPGGSLRLSCAAGPFTSSNAISWVRQAPGKGLEWVRIND-DSTYY	59	
QY	61	NORFGRTTISLDKSKRTAYLQMSLRADIVVYC--ASWISDFPDYNGGGLTVYSSA	118	
Db	60	ADSVAGREFTISRDNAKNTAYLQNLKTEDITAMYYCMDSWASNALDAWGQGLTVYSSSE	119	
QY	119	S	119	
Db	120	S	120	

RESULT 4		
ID	Q9UL90	PRELIMINARY; PRT; 113 AA.
AC	Q9UL90;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)	
DT	01-MAR-2004 (TREMBLrel. 26, last annotation update)	
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
OX	NCBI_TaxID=9606; [1]	
RN		
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=88277139; PubMed=9614934;	
RA	Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,	
RA	Young D.C.;	
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal	
RT	fetus.";	
RT	Clin. Immunol. Immunopathol. 87:184-192(1998).	
DR	EMBL; AF035024; AAD56260.1; -	

```

DR PIR, S78486; S78486.
DR HSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0035; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD1908BD07F CRC64;

Query Match
Best Local Similarity 73.5%; Score 428; DB 2; Length 113;
Matches 86; Conservative 6; Mismatches 21; Indels 4; Gaps 1

OY 1 EVQLVESGGGLVQPGGSLRLSCATGYYFTTEYIIHWVRQAPGKGLHWASINPDYDITNY 60
    |||||
DB 1 EVQLVESGGGVVQPGGSLRLSCAAGFTFSSYGMMHWQAPGKGLHWAFIRYDGSNKRY 60
    |||||

OY 61 NORFGKRTTISLDKSKRTAYLQWNSLRADDTAVYVCASWISDFPDYWGQGLVTYSS 117
    |||||
DB 61 ADVKGRFTTISDNKNTLYLQWNSLRADDTAVYVCARDL----NYWGQGLVTYSS 113
    |||||

RESULT 5
BAD00414 .PRELIMINARY; PRT; 120 AA.
ID BAD00414;
AC BAD00414;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDI region (fragment).
GN IGHV.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Library of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoire.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092052; BAD00414.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 120 AA; 12724 MW; 19D3BE0E07F79949 CRC64;

Query Match
Best Local Similarity 70.3%; Score 428; DB 2; Length 120;
Matches 83; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

OY 2 VOLVESGGGLVQPGGSLRLSCATGYYFTTEYIIHWVRQAPGKGLHWASINPDYDITNY 61
    |||||
DB 2 VOLVESGGGLVQPGGSLRLSCAAGFTFSSYAMSVRQPGKGLERVAINPDGKTYNP 61
    |||||

OY 62 QRFKGRFTTISLDKSKRTAYLQWNSLRADDTAVYVCASWISDFPDYWGQGLVTYSSAS 119
    |||||
DB 62 DSVKGRFTTISDNKNTLYLQWNSLRADDTAVYVCATSSNSVDYWGQGLVTYSSSS 119
    |||||

RESULT 6
O6MZV7 .PRELIMINARY; PRT; 473 AA.
ID O6MZV7;
AC O6MZV7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human small intestine;  
RA THE GERMAN HUMAN CDNA CONSORTIUM;  
RG Bloecher H., Boecher M., Mewes H.W., Well B., Amlid C., Osanger A.,  
RA Fobo G., Han M., Wilmann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BX640853, CAB45920.1; ..  
DR InterPro; IPR003599; IG\_1.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; CI-set; 3.  
DR Pfam; PF00047; IG\_4.  
DR SMART; SM00409; IG\_2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein\_  
SQ SEQUENCE 473 AA; 52121 MW; 9476EAB4C0BFCA47 CR664;

	Query Match	67.4%;	Score 427.5;	DB 2;	Length 473;
	Best Local Similarity	65.1%;	Pred. No. 9.8e-37;		
Dd	Matches 82;	Conservative 13;	Mismatches 24;	Indels 7;	Gaps 1
Oy	1 EVOLVESGGGLVQPGSGRLRSCATSGYTFTEYIIHMVRQAQPKGLEWVASINPDYDITNY 60				
Dd	20 EIQLVESGGGLVQPGSGRLRSLCAASGPFSSFENNVMWRQAQPKGLEWLSIYTRSGNTVYY 79				
Oy	61 NQRKGRPTISLDLSDSKRTAYLQMNSLRADPPVYCA-----SWISDFPVMGGCTLV 113				
Dd	80 ADSIQGRPTISRDNARNSLYIQMNSLRADDPVAVYCANQHHTSPWPSPFDYMGGLIV 139				
Oy	114 TVSSAS 119				
Dd	140 TVSSAS 145				
	RESULT 7				
ID	CAB45920 PRELIMINARY; PRT; 473 AA.				
AC	CAB45920;				
DT	02-MAR-2004 (TrEMBLrel. 27, Created)				
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)				
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)				
Ds	Hypothetical protein DKFP686C11235.				
GN	DKFP686C11235.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Human small intestine;				
RA	Bloecker H., Boecher M., Mewes H.W., Weill B., Amid C., Osanger A.,				
PA	Fobo G., Han M., Wiemann S.;				
RL	Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.				
KR	EMBL, BX640853, CAB45920.1; --				
KM	Hypothetical protein.				
SQ	SEQUENCE 473 AA; 52121 MW; 9476AE4C0BFCA47 CRC64;				
	Query Match	67.4%;	Score 427.5;	DB 2;	Length 473;
	Best Local Similarity	65.1%;	Pred. No. 9.8e-37;		
Matches	82;	Conservative 13;	Mismatches 24;	Indels 7;	Gaps 1
Oy	1 EVOLVESGGGLVQPGSGRLRSCATSGYTFTEYIIHMVRQAQPKGLEWVASINPDYDITNY 60				
Dd	20 EIQLVESGGGLVQPGSGRLRSLCAASGPFSSFENNVMWRQAQPKGLEWLSIYTRSGNTVYY 79				

QY	61	NSGFKRPTISLDKSRRTAYLQMSLRADDTAVYCA-----SWISDPFDYGGOSTLV	113
		:::	
Db	80	ASDLQGRFTTISDNMAANSIYLQMSLRADDTAVYCAQNQHTSPWYSPFDYGGOSTLV	139
QY	114	TVSSAS	119
Db	140	TVSSAS	145

RESULT	8
BAD00406	
ID	BAD00406
AC	BAD00406;
DT	02-MAR-2004 (TrEMBLrel. 27, Created)
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE	Immunoglobulin heavy chain VHDJ region (Fragment).
GN	IGHV.
OS	Camelus dromedarius (Dromedary) (Arabian camel).
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
OX	NCBI_TaxId=9838;
RN	[1]
RP	SEQUENCE FROM N.A.

RT "libraries of heavy-chain antibodies reflecting camel gamma2 and gamma3 in vivo repertoires.";  
RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AB092044; BAD00406.1; -.  
DR EMBL; AB092044; BAD00406.1; -.  
FT NON\_TER 1  
FT NON\_TER 128  
FT NON\_TER 128  
SQ SEQUENCE 128 AA; 13856 MW; 7023CF09C28AB99A CRC64;

	Query Match	67.4%	Score 427;	DB 2:	Length 128;
	Best Local Similarity	66.1%;	Pred. No. 2.5e-37;		
	Matches	84;	Conservative 14;	Mismatches 21;	Indels 8; Gaps 3;
QY	1 EVQLVESGGGLVQPQGSRLRSCATSGYFPTFIYIHWVRQADPKGLEWVASINPDVDITNY	60			
Dd	1 EVLQVESGGGIVQGSGSLRSCAASGFPPSYANNWVRQAQKGLEWVAISNLSGGSGITY	60			
QY	61 NQRKGRFTISLDYSKRTAYIQMNSLRADPTAVYICAS-----WIS-DF-FDIWGQGTLL	112			
Dd	61 ADSVYGRFTISRDNAKTLYLQLINSLKTEDPAMYACADRYRGYRWLSGDYEMDWGKGCTL	120			
QY	113 VTVSAS	119			
Dd	121 VTISSS	127			

RESULT 9			
BAD00444			
ID	BAD00444	PRELIMINARY;	PR1; 128 AA.
AC	BAD00444;		
DT	02-MAR-2004 (TReMBLrel. 27, Created)		
DT	02-MAR-2004 (TReMBLrel. 27, Last sequence update)		
DT	02-MAR-2004 (TReMBLrel. 27, Last annotation update)		
DE	Immunoglobulin heavy chain VHJF region (Fragment).		
GN	ICVH.		
OS	Camelus dromedarius (Dromedary) (Arabian camel).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus		
OX	NB1_Taxid=9838;		
PN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Spleen;		
RA	Honda T., Akahori Y., Kurosawa Y.;		
RT	"Libraries of heavy-chain antibodies reflecting camel gamma2 and		
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB092082; BAD00444.1; -.		
DT	NON_TER 1 1		

PT NON TER 128 128  
SQ SEQUENCE 128 AA; 13775 MW; 059EDD39D9159F3 CRC64;  
Query Match 67.4%; Score 427; DB 2; Length 128;  
Best Local Similarity 66.7%; Pred. No. 2.5e-37;  
Matches 84; Conservative 12; Mismatches 22; Indels 8; Gaps 2;

QY 2 VOLVESGGGLVOPGGSLRLSCATSGYFTETYLIIHMTWQAPGKGLIEMVASINPDYDITNN 61

Db 2 VOLVESGGGLVOPGGSLRLSCATSGFTSSDYMSWVAQPKGLIEMVASINSGGSSTYA 61

QY 62 QREKGRFTIILDKSKRTAYLQNMSLRAEDTAVYYCA-----SWISDF--DYWGQGLV 113

Db 62 DSVKGRFTIIRDNAAKNTILYLNQMSLKEPDIAVYCAITREYGGSHLVGYSNDYNGKGLV 121

QY 114 TVSSAS 119

Db 122 TISSES 127

RESULT 10		
Q9UL71		
ID	Q9UL71	PRELIMINARY; PRT; 121 AA.
AC	Q9UL71;	
DT	01-MAY-2000 (TRENBLrel. 13, Created)	
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)	
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)	
DE	Myosin-reactive immunoglobulin heavy chain variable region (fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
OX	NCBI_TaxId=9606;	

RP	SEQUENCE FROM N.A.
RX	MEDLINE=98277139; Pubmed=9614934;
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA	Young D.C.;
RT	"Wysin-Reactive autoantibodies in rheumatic carditis and normal
RT	fetus." ;
RL	Clin. Immunol. Immunopathol. 87:184-192(1998) .
DR	BMBL; AP035043; AAD56279.1; -.
DR	HSPF, P01852; INED
DR	IncePro; IPR007110; Ig-like.
DR	IncePro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PSS0835; IG LIKE; 1.
FT	NON_TER
FT	NON_TER
QO	SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

[illegible]



DT 02-MAR-2004 (TREMBlrel. 27, Created)  
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
DE Immunoglobulin heavy chain VHJ region (Fragment).  
GN IGVH.  
OS Camelus dromedarius (Dromedary) (Arabian camel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
OX NCBI\_TaxID=9638;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Honda T., Akahori Y., Kurosawa Y.;  
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and  
RT gamma3 in vivo repertoires."  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB092084; BAD00446.1; -.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 122 AA; 13395 MW; 27043ABFC3A4771D CRC64;  
  
Query Match 67.2%; Score 426; DB 2; Length 122;  
Best Local Similarity 67.7%; Pred. No. 3e-37;  
Matches 84; Conservative 10; Mismatches 22; Indels 8; Gaps 2;  
  
QY 1 EVOLVESGGGLVOPGSGRLSCATSGYTFETYYIHMYVQAPGKLEWYASINPDYDITNY 60  
DB 1 DVQLVESGGGLVOPGSGRLSCASGFTFSNYTWVQAPKGLGWVSGINQDSNTYY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLQMSLRAEDTAVVYC-----ASWIDPFYWGQSTLVTV 115  
DB 61 LDSYKGRFTISRDNKNTLYLQMSLSKEDTALYYCAMPYVAGW---FGYWGQSTLVTV 117  
QY 116 SSAS 119  
DB 118 SSES 121  
  
RESULT 12  
BAD00520 PRELIMINARY; PRT; 123 AA.  
AC BAD00520;  
DT 02-MAR-2004 (TREMBlrel. 27, Created)  
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
DE Immunoglobulin heavy chain VHJ region (Fragment).  
GN IGVH.  
OS Camelus dromedarius (Dromedary) (Arabian camel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
OX NCBI\_TaxID=9638;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Honda T., Akahori Y., Kurosawa Y.;  
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and  
RT gamma3 in vivo repertoires."  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB092158; BAD00520.1; -.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 123 AA; 13526 MW; E794FBA8B95C2C3 CRC64;  
  
Query Match 67.1%; Score 425.5; DB 2; Length 123;  
Best Local Similarity 67.2%; Pred. No. 3.4e-37;  
Matches 82; Conservative 14; Mismatches 23; Indels 3; Gaps 1;  
  
QY 1 EVOLVESGGGLVOPGSGRLSCATSGYTFETYYIHMYVQAPGKLEWYASINPDYDITNY 60  
DB 1 EVQLVESGGGLVOPGSGRLSCASGFTFSKFMHWVQAPKGLGWVSGINPVGINITY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLQMSLRAEDTAVVYCASI---SDFPYWGQSTLVTVSS 117  
DB 61 LDSYKGRFTISRDNKNTLYLQMSLSKEDTALYYCAMPYVAGW---FGYWGQSTLVTV 117

DB 61 ADSYKGRFTISRDNKNTLYLQMSLSKEDTALYYCAMPYVAGW---FGYWGQSTLVTVSS 120  
QY 118 AS 119  
DB 121 ES 122  
  
RESULT 13  
AAH06402 PRELIMINARY; PRT; 479 AA.  
AC AAH06402;  
DT 02-MAR-2004 (TREMBlrel. 27, Created)  
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carrincci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,  
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006402; AAH06402.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 479 AA; 52281 MW; D74E0C89082A9788 CRC64;  
  
Query Match 67.1%; Score 425.5; DB 2; Length 479;  
Best Local Similarity 65.2%; Pred. No. 1.6e-36;  
Matches 86; Conservative 10; Mismatches 23; Indels 13; Gaps 1;  
  
QY 1 EVOLVESGGGLVOPGSGRLSCATSGYTFETYYIHMYVQAPGKLEWYASINPDYDITNY 60  
DB 20 EVQLVESGGGLVOPGSGRLSCASGFTFSKFMHWVQAPKGLGWVSGINQDSNTYY 79  
QY 61 NQRFKGRFTISLDKSKRTAYLQMSLRAEDTAVVYCASI---SDFPYWGQSTLVTVSS 107  
DB 80 ADSYKGRFTISRDNKNTLYLQMSLSKEDTALYYCAMPYVAGW---FGYWGQSTLVTVSS 139  
QY 108 GQGLTVTVSSAS 119  
DB 140 GQGLTVTVSSAS 151  
  
RESULT 14  
Q8WUK1 PRELIMINARY; PRT; 613 AA.  
AC Q8WUK1;  
Q8WUK1

DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE IGHM protein.  
DE Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Alechski S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marustina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stepienon M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carrino P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalon D.K., Mizny D.N., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL, BC020240; AAH20240.1; -.  
DR PIR, F36005; F36005.  
DR PIR, G36005; G36005.  
DR PIR, PH1642; PH1642.  
DR PIR, PH1643; PH1643.  
DR PIR, PH1645; PH1645.  
DR PIR, PH1646; PH1646.  
DR PIR, PL0098; PL0098.  
DR PIR, PL0120; PL0120.  
DR PIR, S15590; S15590.  
DR PIR, S11116; S11116.  
DR PIR, S31119; S31119.  
DR PIR, S70442; S70442.  
DR HSP, P01861; IADO.  
DR InterPro; IPRO07110; IG\_1like.  
DR InterPro; IPRO03597; IG\_cl.  
DR InterPro; IPRO03006; IG\_MHC.  
DR InterPro; IPRO03596; IG\_v.  
DR Pfam; PF07654; Cl-set; 4.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671B315 CRC64;

Query Match	67.0%	Score 424.5	DB 2	Length 613
Beet Local Similarity	70.5%	Pred. No. 2.8e-36		
Matches	86	Conservative 8	Mismatches 25	Indels 3
			Gaps 2	
Qy	1	EVQVIESGGVLVQPGSGRLSCATSGYPTFTETIHHMWQAQPKGLEWVASINPDYDINNY	60	
	:			
Db	20	QVQVIESGGGVQVQPSRLSLSCAAGPFTFSSGMMHWQAQPKGLEWVAIVSYDSNKKY	79	
	:			
Qy	61	NQRFKGRFTSLDCKRKTAYVLOMNSLRADTAVVYCA-SWIS--DFPDWGGCTLVWYS	117	
	:			
Db	80	ADSVAGRFTSLSDNSKNLTVLOMNSLRADTAVVYCAQDMSGSGVTFDIDWGGINVTSS	139	
	:			

QY	118 AS	119
Db	140 GS	141

RESULT 15	
BAD00531	
ID	BAD00531
AC	BAD00531
DT	02-MAR-2004 (TREMblrel. 27, Created)
DT	02-MAR-2004 (TREMblrel. 27, Last sequence update)
DT	02-MAR-2004 (TREMblrel. 27, Last annotation update)
DE	Immunoglobulin heavy chain VHJ3 region (Fragment).
GN	IGHV.
OS	Camelus dromedarius (Dromedary) (Arabian camel).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX	NCBI_TaxID=9838;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISUE=Splice;
RA	Honda T., Akahori Y., Kurosawa Y.;
RT	"Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT	gamma3 in vivo repertoires.";
RL	Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
DR	EMBL; AB092169; BAD00531.1; -.
FT	NON_TER 1
FT	NON_TER 1
SO	SEQUENCE 120 AA; 1327 MW; 8DB4F604E7677FAB CRC64;

[illegible]

Search completed: December 29, 2004, 19:31:33  
Job time : 133.79 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	446	70.3	135	2	S31598	Ig heavy chain V r
2	442	69.7	119	2	S31107	Ig heavy chain - h
3	438	69.1	119	2	D36005	Ig heavy chain V r
4	437	68.9	119	2	C36005	Ig heavy chain V r
5	436.5	68.8	124	2	S20782	Ig heavy chain V r
6	436	68.8	121	2	G36005	Ig heavy chain V r
7	436	68.8	123	2	S31114	Ig heavy chain - h
8	436	68.8	140	2	S31686	Ig heavy chain - h
9	435	68.6	119	2	S31108	Ig heavy chain V r
10	435	68.6	132	2	S31603	Ig heavy chain V r
11	434.5	68.5	114	2	S46390	Ig heavy chain V r
12	434.5	68.5	120	2	S48798	Ig heavy chain V r
13	434	68.5	140	2	S31588	Ig heavy chain V r
14	433.5	68.4	128	2	S26786	Ig heavy chain V r
15	433.5	68.4	140	2	S70442	Ig heavy chain pre
16	433	68.3	125	2	S30531	Ig heavy chain V r
17	431	68.0	134	2	S31639	Ig heavy chain V r
18	429	67.7	121	2	S19666	Ig heavy chain V r
19	428.5	67.6	120	2	S44111	Ig heavy chain V r
20	428.5	67.6	137	2	S31701	Ig heavy chain V-E
21	428	67.5	119	2	F36005	Ig heavy chain V r
22	427.5	67.4	114	2	S46381	Ig heavy chain V r
23	427.5	67.4	136	2	S31587	Ig heavy chain V r
24	427	67.4	138	2	S31666	Ig heavy chain V r
25	425	67.0	140	2	A30532	Ig heavy chain V r
26	425	67.0	143	2	S23634	Ig heavy chain pre
27	424.5	66.9	122	2	S31117	Ig heavy chain - h
28	424	66.9	130	2	S31601	Ig heavy chain V r
29	423.5	66.8	120	2	S31112	Ig heavy chain - h

30	422.5	66.6	147	2	137780	1g variable region
31	422	66.6	117	2	578486	1g heavy chain V <sub>H</sub> I
32	422	66.6	134	2	531679	1g heavy chain V <sub>H</sub> I
33	421.5	66.5	114	2	531120	1g heavy chain - I
34	421	66.4	120	2	536273	1g heavy chain V <sub>H</sub> I
35	421	66.4	121	2	531118	1g heavy chain - I
36	420	66.2	121	2	155673	1g heavy chain - I
37	418	65.9	127	2	538489	1g heavy chain - I
38	417.5	65.8	122	2	520772	1g heavy chain V <sub>H</sub> I
39	417	65.8	121	2	531104	1g heavy chain (S <sub>H</sub> )
40	417	65.8	160	2	505271	1g heavy chain pre
41	416.5	65.7	118	2	531105	1g heavy chain (S <sub>H</sub> )
42	416.5	65.7	122	2	531675	1g heavy chain V <sub>H</sub> I
43	416.5	65.7	141	2	531669	1g heavy chain V <sub>H</sub> I
44	415.5	65.5	122	2	569910	1g V-D-J region (H <sub>1</sub> )
45	415.5	65.5	151	2	A60943	1g heavy chain pre

## ALIGNMENTS

## RESULT 1

531598  
 Ig heavy chain V region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S31598  
 R/Chisnister, A.W.; Gauchier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A/Accession: S31598  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-135 <CUI>  
 A/Cross-references: EMBL:Z14170; NID:G31001; PIDN:CAA76539.1; PID:G31002  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 C/31-114/Domain: immunoglobulin homology <IMM>

Query Match	70.3%	Score 446;	DB 2;	Length 135;
Best Local Similarity	74.8%;	Pred. No. 2.2e-34;		
Matches 89;	Conservative	5;	Mismatches 23;	Indels 2;
				Gaps 1.

QY 1 EVQVLSGGGLVQPGGSLRLSCATSSYTTETETI IHHVROA PGKGLFWASINPDIDITNY 68  
Db 17 QVQLVSSGGGAVQPGGSLRLSCAASEPTSSSGMHVRRQAPGGGLFWAPAIRDGSNKRY 76  
QY 61 NQRFKRPFTISLDKSRRTAYLQNNISIRAPDAVYCA--SWISDFPDYWGQGLTVTSS 117  
Db 77 ADSVKRPFITSRNSKNITLYLQNNISIRADIAVYCAKISWEVSRDYWGQGLTVTSS 139

## RESULT 2

ig heavy chain human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C/Accession: S31107  
R/Rapaport, F.M.; Tlimer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A/TITLE: Restricted utilization of germ-line VH3 genes and short diverse third comple  
A/Reference number: S31104; MUID:92111633; PMID:1170252  
A/Accession: S31107  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-119 <RAA>  
A/Cross-references: EMBL:X62955  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
C/15-98/Domain: immunoglobulin homology <IM>

```
Query Match          69.7%; Score 442; DB 2; Length 119;
Best Local Similarity 73.9%; Pred. No. 4.5e-34;
Matches 88; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NORFKGRFTISLDKSKRTAYLQNSLRABDTAVYYCA--WISDFPDYWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADVKGRFTISRDNKNTLYLQNSLRABDTAVYYCAKDPGASTYFPDYWGQGLTVTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
D36005
Ig heavy chain V region (M43) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: D36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: D36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: GB:M34024
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          69.1%; Score 438; DB 2; Length 119;
Best Local Similarity 72.3%; Pred. No. 1.1e-33;
Matches 86; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NORFKGRFTISLDKSKRTAYLQNSLRABDTAVYYCA--WISDFPDYWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADVKGRFTISRDNKNTLYLQNSLRABDTAVYYCAKKQNDWDFPDYWGQGLTVTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
C36005
Ig heavy chain V region (30p1) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C/Accession: C36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: C36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: GB:M18513
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          68.9%; Score 437; DB 2; Length 119;
Best Local Similarity 73.3%; Pred. No. 1.3e-33;
Matches 88; Conservative 7; Mismatches 21; Indels 4; Gaps 2;

QY 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
DB 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NORFKGRFTISLDKSKRTAYLQNSLRABDTAVYYCA--ASWISDFPDYWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADVKGRFTISRDNKNTLYLQNSLRABDTAVYYCAKDPGASTYFPDYWGQGLTVTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S20782
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C/Accession: S20782
R/Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A/Description: Analysis of the Igh and Igg rearranged VH repertoire of human cord blood
A/Reference number: S20765
A/Accession: S20782
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-124 <MOR>
A/Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          68.8%; Score 436.5; DB 2; Length 124;
Best Local Similarity 69.4%; Pred. No. 1.5e-33;
Matches 86; Conservative 10; Mismatches 21; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NORFKGRFTISLDKSKRTAYLQNSLRABDTAVYYCA-----WISDFPDYWGQGLTV 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADVKGRFTISRDNKNTLYLQNSLRABDTAVYYCAKAKRIALFVAVIPHFDPYWGQGLTV 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 114 TVSS 117
    |||||
DB 121 TVSS 124
    |||||

RESULT 6
G36005
Ig heavy chain V region (M74) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C/Accession: G36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: G36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-121 <SCH>
A/Cross-references: UNIPROT:Q8WUK1; GB:M34031
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          68.8%; Score 436; DB 2; Length 121;
Best Local Similarity 71.9%; Pred. No. 1.6e-33;
Matches 87; Conservative 6; Mismatches 24; Indels 4; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVOLVESGGGLVPGGSLRLSCLATGTYFTETIIHWVRAQPGKLEWVASINPDYDITNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 1 QVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASISYDGSNKYY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLQNMSLRADPTAVYYCA-----SWISDFPDYWGQGLTVTVSS 116  
Db 61 ADSVKGRTTISRDNSKNTLYLQNMSLRADPTAVYYCAKDRKDMGALPDYWGQGLTVTVSS 120  
QY 117 S 117  
Db 121 S 121

## RESULT 7

S3114  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C/Accession: S31114  
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A/Reference number: S31104; MUID:92111633; PMID:1730252  
A/Accession: S31114  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-123 <RAA>  
A/Cross-references: EMBL:X62963  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 436; DB 2; Length 123;  
Best Local Similarity 69.0%; Pred. No. 1.7e-33;  
Matches 87; Conservative 8; Mismatches 19; Indels 12; Gaps 2;

QY 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASINPDYDITNY 60  
Db 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASISGSGGTTY 60

QY 61 NQRFKGRFTISLDKSKRTAYLQNMSLRADPTAVYYCA-----SWISDFPDYWGQGLTVTVSS 111  
Db 61 ADSVKGRTTISRDNSKNTLYLQNMSLRADPTAVYYCAKASLYLRLEWL---FDYWGQGLTVTVSS 117

QY 112 LVTYSS 117  
Db 118 LVTYSS 123

## RESULT 8

S31686  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31686  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31686  
A/Molecule type: mRNA  
A/Status: preliminary  
A/Residues: 1-140 <CUI>  
A/Cross-references: EMBL:Z14205; NID:930969; PIDN:CA78574.1; PID:930970  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 436; DB 2; Length 140;  
Best Local Similarity 71.9%; Pred. No. 1.9e-33;  
Matches 87; Conservative 9; Mismatches 21; Indels 4; Gaps 1;

QY 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASINPDYDITNY 60  
Db 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASISGSGGTTY 60

Db 20 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASISGSGGTTY 79  
QY 61 NQRFKGRFTISLDKSKRTAYLQNMSLRADPTAVYYCA-----SWISDFPDYWGQGLTVTVSS 116  
Db 80 SDSVKGRTTISRDNSKNTLYLQNMSLRADPTAVYYCAKCPGAGSPSPDYWGQGLTVTVSS 139  
QY 117 S 117  
Db 140 S 140

## RESULT 9

S31108  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C/Accession: S31108  
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma  
Eur. J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A/Reference number: S31104; MUID:92111633; PMID:1730252  
A/Accession: S31108  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-119 <RAA>  
A/Cross-references: EMBL:X62956  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 435; DB 2; Length 119;  
Best Local Similarity 72.3%; Pred. No. 2e-33;  
Matches 86; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASINPDYDITNY 60  
Db 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASISGSGGTTY 60

QY 61 NQRFKGRFTISLDKSKRTAYLQNMSLRADPTAVYYCA-----SWISDFPDYWGQGLTVTVSS 117  
Db 61 ADSVKGRTTISRDNSKNTLYLQNMSLRADPTAVYYCAKDRKRLTGTFDYWGQGLTVTVSS 119

## RESULT 10

S31603  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31603  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31603  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-132 <CUI>  
A/Cross-references: EMBL:Z14168; NID:930999; PIDN:CA78537.1; PID:931000  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F,30-113/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 435; DB 2; Length 132;  
Best Local Similarity 72.6%; Pred. No. 2.2e-33;  
Matches 85; Conservative 8; Mismatches 24; Indels 0; Gaps 0;

QY 1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASINPDYDITNY 60  
Db 16 EVQLVESGGGVVQPGGSLRLSCAASGFTFSISYAMHWRAQAPGKGLIEWVASISYDGSNKYY 75  
QY 61 NQRFKGRFTISLDKSKRTAYLQNMSLRADPTAVYYCAKASISDFPDYWGQGLTVTVSS 117  
Db 61 NQRFKGRFTISLDKSKRTAYLQNMSLRADPTAVYYCAKASISDFPDYWGQGLTVTVSS 117



C:Species: Homo sapiens (man)  
 C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C:Accession: S70442  
 R:Contributor: A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.  
 MOL: Immunol. 29, 1363-1373, 1992  
 A:Title: Igm kappa/lambda Ekv human B cell clone: an early step of differentiation of fe  
 A:Reference number: S70442; MUID:93024508; PMID:1383695  
 A:Accession: S70442  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-140 <CUI>  
 A:Cross-references: UNIPROT:Q8WUK1  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 68.4%; Score 433.5; DB 2; Length 140;

Best local Similarity 72.5%; Pred. No. 3.3e-33; Matches 87; Conservative 7; Mismatches 23; Indels 3; Gaps 1;

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QY      1  EVQLVESGGGLVQPGGSLRLSCATGSGYTFETEIIMHWROAPGKGLWVAISINPDYDITNY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      20  QVQLVESGGGVVQPGGSLRLSCAASGFTFSNYGMHWROAPGKGLWVAFIRYDGSNKYY 79
QY      61  NQRFKGRFTISLDKSKRTAYLQMNSLRADTAIVYYCAS---WISDFPYMGCGTIVTVSS 117
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      80  ADSYKGRFTISRDNKNTLYLQMNSLRADTAIVYYCARDHIVGATYFDYMGCGTIVTVSS 139

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Search completed: December 29, 2004, 19:36:35

Job time : 26.0258 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 29, 2004, 19:36:01 ; Search time 98.0601 Seconds  
(without alignments)  
436.545 Million cell updates/sec

Title: US-10-044-896-5

Perfect score: 634  
Sequence: 1 EVLVSSGGGLVQPGSLRL.....ISDFYWGQGLTWVSAS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep:\*  
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7: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	634	100.0	119	US-10-044-896-5	Sequence 5, Appl1
2	499.5	78.8	232	US-09-811-384-10	Sequence 10, Appl1
3	499.5	78.8	232	US-10-404-286-10	Sequence 10, Appl1
4	499.5	78.8	241	US-09-940-166A-1	Sequence 1, Appl1
5	499.5	78.8	241	US-10-762-967-1	Sequence 1, Appl1
6	499.5	78.8	300	US-09-940-166A-7	Sequence 7, Appl1
7	499.5	78.8	300	US-10-227-694-2	Sequence 2, Appl1
8	499.5	78.8	300	US-10-762-967-7	Sequence 2, Appl1
9	499.5	78.8	450	US-09-811-384-12	Sequence 12, Appl1
10	499.5	78.8	450	US-10-404-286-12	Sequence 12, Appl1
11	499.5	78.8	469	US-10-835-641-23	Sequence 23, Appl1
12	493	77.8	119	US-10-044-896-2	Sequence 2, Appl1
13	492.5	77.7	452	US-10-818-765-4	Sequence 4, Appl1

14	487	76.8	119	US-09-811-123-2	Sequence 2, Appl1
15	487	76.8	119	US-10-268-501-4	Sequence 4, Appl1
16	487	76.8	119	US-10-608-626-4	Sequence 4, Appl1
17	487	76.8	119	US-10-600-152-13	Sequence 13, Appl1
18	487	76.8	119	US-10-619-754-4	Sequence 4, Appl1
19	487	76.8	119	US-10-719-310-4	Sequence 4, Appl1
20	484.5	76.4	122	US-10-818-765-2	Sequence 2, Appl1
21	481	75.9	451	US-10-423-299-4	Sequence 4, Appl1
22	480.5	75.8	122	US-10-835-641-20	Sequence 20, Appl1
23	477.5	75.3	253	US-09-726-258-52	Sequence 52, Appl1
24	477.5	75.3	253	US-09-726-258-55	Sequence 55, Appl1
25	477.5	75.3	256	US-09-726-258-70	Sequence 70, Appl1
26	477.5	75.3	298	US-09-726-258-60	Sequence 60, Appl1
27	477.5	75.3	452	US-09-726-258-71	Sequence 71, Appl1
28	473	74.6	121	US-09-795-798-5	Sequence 5, Appl1
29	470	74.1	121	US-09-795-798-24	Sequence 24, Appl1
30	468.5	73.9	122	US-10-835-641-26	Sequence 26, Appl1
31	463	73.0	225	US-10-364-953-12	Sequence 12, Appl1
32	463	73.0	225	US-10-364-953-17	Sequence 17, Appl1
33	463	73.0	470	US-10-020-786-9	Sequence 9, Appl1
34	463	73.0	470	US-10-267-286A-13	Sequence 13, Appl1
35	462	72.9	119	US-10-267-286A-14	Sequence 14, Appl1
36	461.5	72.8	228	US-10-253-366-2	Sequence 2, Appl1
37	461.5	72.8	449	US-10-356-974-2	Sequence 2, Appl1
38	461.5	72.8	449	US-10-423-299-2	Sequence 2, Appl1
39	461.5	72.8	449	US-10-659-825-2	Sequence 2, Appl1
40	461.5	72.8	449	US-10-723-003-54	Sequence 54, Appl1
41	461.5	72.8	449	US-10-182-975-25	Sequence 25, Appl1
42	461.5	72.8	527	US-10-723-003-58	Sequence 58, Appl1
43	461.5	72.8	628		
44	461.5	72.8			
45	461.5	72.8			

#### ALIGNMENTS

RESULT 1  
US-10-044-896-5  
; Sequence 5, Application US/10044896  
; Publication No. US2003016228A1  
; GENERAL INFORMATION:  
; APPLICANT: Chantharapai, Anan  
; APPLICANT: Kim, Jin K.  
; APPLICANT: Stewart, Timothy  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES  
; FILE REFERENCE: GENENT. 074A  
; CURRENT APPLICATION NUMBER: US/10/044, 896  
; CURRENT FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: 60/270775  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: This sequence represents a humanized chimeric antibody comprising human and non-human sequences.  
US-10-044-896-5

Query Match 100.0%; Score 634; DB 14; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.8e-50;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVSSGGGLVQPGSLRLSCATSGTFTYIHWRAQPGKGLWVASINDYITNY 60  
DB 1 EVLVSSGGGLVQPGSLRLSCATSGTFTYIHWRAQPGKGLWVASINDYITNY 60  
QY 61 NORFKRFTSLDKSKRTAYLQNSLRADTAVYGCASMSDFYWGQGLTWVSAS 119



ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940.166A  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097.309  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-940-166A-1  
Query Match 78.8%; Score 499.5; DB 9; Length 241;  
Best Local Similarity 77.0%; Pred. No. 7.6e-38;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
QY 1 EVQLVESGGGLVQPGGSLRLSCATGFTFEYTHHWRAQPGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCATGFTFEYTHHWRAQPGKLEWVASINPDYDITNY 60  
QY 61 NORFKRFTTSLDLSKRTAVLQWNSLRADTAAYVYCASWIS-----DFPDYGCGTLV 113  
DB 61 NORFKRFTTSLDLSKRTAVLQWNSLRADTAAYVYCASWIS-----DFPDYGCGTLV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
RESULT 5  
US-10-762-967-1  
Sequence 1, Application US/10762967  
Publication No. US20040138426A1  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 09/097.309  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-762-967-1

APPLICATION NUMBER: US/10/762.967  
FILING DATE: 21-Jan-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/097.309  
FILING DATE: 12-Jun-1998  
APPLICATION NUMBER: 60/050951  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-762-967-1  
Query Match 78.8%; Score 499.5; DB 16; Length 241;  
Best Local Similarity 77.0%; Pred. No. 7.6e-38;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
QY 1 EVQLVESGGGLVQPGGSLRLSCATGFTFEYTHHWRAQPGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCATGFTFEYTHHWRAQPGKLEWVASINPDYDITNY 60  
QY 61 NORFKRFTTSLDLSKRTAVLQWNSLRADTAAYVYCASWIS-----DFPDYGCGTLV 113  
DB 61 NORFKRFTTSLDLSKRTAVLQWNSLRADTAAYVYCASWIS-----DFPDYGCGTLV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
RESULT 6  
US-09-940-166A-7  
Sequence 7, Application US/09940166A  
Patent No. US20020058324A1  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940.166A  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097.309  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 300 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-940-166A-7

Query Match      78.8%; Score 499.5; DB 9; Length 300;
Best Local Similarity 77.0%; Pred. No. 9.5e-38;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDITNY 60
    |||||
DB 24 EVOLVESGGGLVPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGSTSH 83
    |||||

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRABDTAVYYCASWIS-----DFPDYWGQGLTV 113
    |||||
DB 84 NORFMDFRTISVDKSTSTAYMQWNSLRABDTAVYYCARWRGLNYGPDVRYFDWVGQGLTV 143
    |||||

QY 114 TVSSAS 119
    |||||
DB 144 TVSSAS 149

RESULT 7
US-10-227-694-2
; Sequence 2, Application US/10227694
; Publication No. US2003007739A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; APPLICANT: Andersen, Dana
; TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
; FILE REFERENCE: P1867R1
; CURRENT APPLICATION NUMBER: US/10/227,694
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/315,209
; PRIOR FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-227-694-2

Query Match      78.8%; Score 499.5; DB 14; Length 300;
Best Local Similarity 77.0%; Pred. No. 9.5e-38;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDITNY 60
    |||||
DB 24 EVOLVESGGGLVPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGSTSH 83
    |||||

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRABDTAVYYCASWIS-----DFPDYWGQGLTV 113
    |||||
DB 84 NORFMDFRTISVDKSTSTAYMQWNSLRABDTAVYYCARWRGLNYGPDVRYFDWVGQGLTV 143
    |||||

QY 114 TVSSAS 119
    |||||
DB 144 TVSSAS 149

RESULT 8
US-10-762-967-7
; Sequence 7, Application US/10762967
; Publication No. US20040138426A1
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
```

```
; Narindray, Daljit S.
; Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/762,967
; FILING DATE: 21-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; APPLICATION NUMBER: 60/050951
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 300 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-762-967-7

Query Match      78.8%; Score 499.5; DB 16; Length 300;
Best Local Similarity 77.0%; Pred. No. 9.5e-38;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATSGYTFEYIIHWVROAPGKGLEWVASINPDYDITNY 60
    |||||
DB 24 EVOLVESGGGLVPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGSTSH 83
    |||||

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRABDTAVYYCASWIS-----DFPDYWGQGLTV 113
    |||||
DB 84 NORFMDFRTISVDKSTSTAYMQWNSLRABDTAVYYCARWRGLNYGPDVRYFDWVGQGLTV 143
    |||||

QY 114 TVSSAS 119
    |||||
DB 144 TVSSAS 149

RESULT 9
US-09-811-384-12
; Sequence 12, Application US/09811384
; Patent No. US20020081294A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Grose, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
```

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/811,384  
FILING DATE: 20-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/251652  
FILING DATE: 17-FEB-2000  
APPLICATION NUMBER: 08/788800  
FILING DATE: 22-JAN-1997  
APPLICATION NUMBER: 60/093038  
FILING DATE: 23-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1729C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-811-384-12

Query Match 78.8%; Score 499.5; DB 9; Length 450;  
Best Local Similarity 77.0%; Pred. No. 1.4e-37;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYFTFYIHWMVROAPGKGLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCATGYFTFYIHWMVROAPGKGLEWVASINPDYDITNY 60  
QY 61 NQREKGFRTSLDKSKRTAVLQNMNLSRAEDTAVVYCAWSIS-----DFPDYWGQGLTV 113  
DB 61 NQRFMDFTTISVDKSTSTAVYQNMNLSRAEDTAVVYCAWMGLNVPDVRFTDVGQGLTV 120

QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 10  
US-10-404-286-12  
Sequence 12, Application US/10404286  
Publication No. US20040057951A1  
GENERAL INFORMATION:  
APPLICANT: Bednar, Martin M.  
Thomas, G. Roger  
Grosb, Cordell E.  
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/404,286

FILING DATE: 31-Mar-2006  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/811384  
FILING DATE: 20-DEC-2000  
APPLICATION NUMBER: 09/251652  
FILING DATE: 17-FEB-2000  
APPLICATION NUMBER: 08/788800  
FILING DATE: 22-JAN-1997  
APPLICATION NUMBER: 60/093038  
FILING DATE: 23-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, David W.  
REGISTRATION NUMBER: NONE  
REFERENCE/DOCKET NUMBER: P1729C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1739  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-404-286-12

Query Match 78.8%; Score 499.5; DB 15; Length 450;  
Best Local Similarity 77.0%; Pred. No. 1.4e-37;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYFTFYIHWMVROAPGKGLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCATGYFTFYIHWMVROAPGKGLEWVASINPDYDITNY 60  
QY 61 NQREKGFRTSLDKSKRTAVLQNMNLSRAEDTAVVYCAWSIS-----DFPDYWGQGLTV 113  
DB 61 NQRFMDFTTISVDKSTSTAVYQNMNLSRAEDTAVVYCAWMGLNVPDVRFTDVGQGLTV 120

QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 11  
US-10-835-641-23  
Sequence 23, Application US/10835641  
Publication No. US20040236078A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
Presta, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/835,641  
FILING DATE: 30-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/705,398  
FILING DATE: 02-Nov-2000  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993

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; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lee, Wendy M.
;   REGISTRATION NUMBER: 40,378
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650/225-1994
;     TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 23:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 469 amino acids
;       TYPE: Amino Acid
;       TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-835-641-23
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Query Match      78.8%; Score 499.5; DB 17; Length 469;
Best Local Similarity 77.0%; Pred. No. 1.5e-37;
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;
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QY 1 EVOLVESGGGLVOPGGSRLRSCATSGYTFTEYIIHWVROAPGKGLWVVASINPDYDITNY 60
    |||||
DB 20 EVOLVESGGGLVOPGGSRLRSCATSGYTFTEYIIHWVROAPGKGLWVAGINPNKGTSH 79
    |||||
QY 61 NORFKGRFTISLDKSKRTAYLQNNLSRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113
    |||||
DB 80 NORFKGRFTISVDKSTSTAYLQNNLSRAEDTAVYYCARMGVNGFDPVRFPDWGQGLTV 139
    |||||
QY 114 TVSSAS 119
    |||||
DB 140 TVSSAS 145
```

```

RESULT 12
; Sequence 2, Application US/10044896
; Publication No. US20030166228A1
; GENERAL INFORMATION:
;   APPLICANT: Chuntharapai, Anan
;   APPLICANT: Kim, Jin K.
;   APPLICANT: Stewart, Timothy
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
;   FILE REFERENCE: GENENT.074A
;   CURRENT APPLICATION NUMBER: US/10/044,896
;   CURRENT FILING DATE: 2002-01-09
;   PRIOR APPLICATION NUMBER: 60/270775
;   PRIOR FILING DATE: 2001-02-22
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Murine
US-10-044-896-2
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```

Query Match      77.8%; Score 493; DB 14; Length 119;
Best Local Similarity 73.1%; Pred. No. 1.4e-37;
Matches 87; Conservative 17; Mismatches 15; Indels 0; Gaps 0;
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```

QY 1 EVOLVESGGGLVOPGGSRLRSCATSGYTFTEYIIHWVROAPGKGLWVVASINPDYDITNY 60
    |||||
DB 1 EVOLVQSGGPELVAFPGASVKISCKTSGYTFTEYIIHWKQGHGSLSEMTGISINPDYDITNY 60
    |||||
QY 61 NORFKGRFTISLDKSKRTAYLQNNLSRAEDTAVYYCASWISDFPDYWGQGLTVSSAS 119
    |||||
DB 61 NORFKGRFTISLDKSKRTAYLQNNLSRAEDTAVYYCASWISDFPDYWGQGLTVSSAS 119
    |||||
```

```

RESULT 13
US-10-818-765-4
; Sequence 4, Application US/10818765
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; Publication No. US20040202658A1
; GENERAL INFORMATION:
;   APPLICANT: Benayahu, Mark C.
;   TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
;   TITLE OF INVENTION: INADEQUATE RESPONSE TO A TNF- $\alpha$  INHIBITOR
;   FILE REFERENCE: P2027R1-US
;   CURRENT APPLICATION NUMBER: US/10/818,765
;   CURRENT FILING DATE: 2004-04-06
;   PRIOR APPLICATION NUMBER: US 60/461,4819
;   PRIOR FILING DATE: 2003-04-09
;   NUMBER OF SEQ ID NOS: 4
;   SEQ ID NO 4
;   LENGTH: 452
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized sequence
US-10-818-765-4
```

```

Query Match      77.7%; Score 492.5; DB 17; Length 452;
Best Local Similarity 76.4%; Pred. No. 6.3e-37;
Matches 97; Conservative 6; Mismatches 13; Indels 11; Gaps 2;
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```

QY 1 EVOLVESGGGLVOPGGSRLRSCATSGYTFTEYIIHWVROAPGKGLWVVASINPDYDITNY 60
    |||||
DB 1 EVOLVESGGGLVOPGGSRLRSCASGYTFETSYNMHWVROAPGKGLWVAGIYPGNGDTSY 60
    |||||
QY 61 NORFKGRFTISLDKSKRTAYLQNNLSRAEDTAVYYCASWIS-----WISDFPDYWGQGLTV 112
    |||||
DB 61 NORFKGRFTISVDKSKRTAYLQNNLSRAEDTAVYYCARVYYVSYNSYW---YFPDWGQGLTV 117
    |||||
QY 113 TVSSAS 119
    |||||
DB 118 TVSSAS 124
```

```

RESULT 14
US-09-811-123-2
; Sequence 2, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
;   APPLICANT: Sharon Erickson
;   APPLICANT: Ralph Schwall
;   APPLICANT: Mark Silkowski
;   TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-BrB
;   TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
;   FILE REFERENCE: GENENT.073A2
;   CURRENT APPLICATION NUMBER: US/09/811,123
;   CURRENT FILING DATE: 2001-03-16
;   PRIOR APPLICATION NUMBER: 60/238,327
;   PRIOR FILING DATE: 2000-10-05
;   PRIOR APPLICATION NUMBER: 09/602,530
;   PRIOR FILING DATE: 2000-06-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-2
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```

Query Match      76.8%; Score 487; DB 9; Length 119;
Best Local Similarity 78.2%; Pred. No. 5.1e-37;
Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;
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```

QY 1 EVOLVESGGGLVOPGGSRLRSCATSGYTFTEYIIHWVROAPGKGLWVVASINPDYDITNY 60
    |||||
DB 1 EVOLVESGGGLVOPGGSRLRSCASGYTFETDYMVROAPGKGLWVADVNSGGSITV 60
    |||||
QY 61 NORFKGRFTISLDKSKRTAYLQNNLSRAEDTAVYYCASWIS--SDFPDYGQGLTVVSS 117
    |||||
```

Db 61 NORFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVVYVCANNLGPSPFYFDYWGQGLVTVSS 119

RESULT 15

US-10-268-501-4  
 / Sequence 4, Application US/10268501  
 / Publication No. US20030086924A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Sliwowski, Mark X.  
 / TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies  
 / FILE REFERENCE: P1467R2P1  
 / CURRENT APPLICATION NUMBER: US/10/268,501  
 / PRIOR FILING DATE: 2002-10-10  
 / PRIOR APPLICATION NUMBER: US 09/602,812  
 / PRIOR FILING DATE: 2000-06-23  
 / PRIOR APPLICATION NUMBER: US 60/141,316  
 / PRIOR FILING DATE: 1999-06-25  
 / NUMBER OF SEQ ID NOS: 13  
 / SEQ ID NO 4  
 / LENGTH: 119  
 / TYPE: PRT  
 / ORGANISM: Artificial sequence  
 / FEATURE:  
 / OTHER INFORMATION: Humanized VH sequence  
 US-10-268-501-4

Query Match 76.8%; Score 487; DB 14; Length 119;  
 Best Local Similarity 78.2%; Pred. No. 5.1e-37;  
 Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCATSGYTFETEIIMWVRQAPGKGLEWVASINPDYDITNY 60  
 |||||  
 Db 1 EVOLVESGGGLVQPGGSLRLSCATSGYTFETDIYMDVNRQAPGKGLEWVADVNPNSGGSIT 60  
 |||||  
 QY 61 NORFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVVYVCANNLGPSPFYFDYWGQGLVTVSS 117  
 |||||  
 Db 61 NORFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVVYVCANNLGPSPFYFDYWGQGLVTVSS 119  
 |||||

Search completed: December 29, 2004, 19:52:40  
 Job time : 99.0601 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 19:21:17 / Search time 28.6009 Seconds  
(without alignments)  
275.930 Million cell updates/sec

Title: US-10-044-896-5  
Perfect score: 634  
Sequence: 1 EVOLVESGGGLVQPGGSLRL.....ISDFPDYWGQGTIVTVSSAS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	503.5	79.4	232	2	US-07-934-373C-27
2	503.5	79.4	232	3	US-08-437-642B-27
3	503.5	79.4	232	5	PCT-US93-07832-27
4	499.5	78.8	232	2	US-07-934-373C-29
5	499.5	78.8	232	2	US-08-788-800-10
6	499.5	78.8	232	3	US-08-437-642B-29
7	499.5	78.8	232	5	PCT-US93-07832-29
8	499.5	78.8	235	2	US-07-934-373C-30
9	499.5	78.8	235	5	US-08-437-642B-30
10	499.5	78.8	235	5	PCT-US93-07832-30
11	499.5	78.8	241	3	US-09-097-309-1
12	499.5	78.8	241	3	US-09-097-171A-1
13	499.5	78.8	241	3	US-09-460-587-1
14	499.5	78.8	241	4	US-09-940-166A-1
15	499.5	78.8	300	3	US-09-097-309-7
16	499.5	78.8	300	3	US-09-097-171A-11
17	499.5	78.8	300	3	US-09-422-712B-3
18	499.5	78.8	300	3	US-09-607-756-3
19	499.5	78.8	300	4	US-09-940-166A-7
20	499.5	78.8	450	2	US-08-788-800-12
21	499.5	78.8	469	2	US-07-934-373C-23
22	499.5	78.8	469	3	US-08-437-642B-23
23	499.5	78.8	469	4	US-08-146-206C-23
24	499.5	78.8	469	4	US-09-705-686-23
25	499.5	78.8	469	4	US-09-705-392A-23
26	499.5	78.8	552	5	PCT-US93-07832-23
27	499.5	78.8	552	5	PCT-US93-07832-23

28	498.5	78.6	232	2	US-07-934-373C-28	Sequence 28, Appl
29	498.5	78.6	232	3	US-08-437-642B-28	Sequence 28, Appl
30	498.5	78.6	232	5	PCT-US93-07832-28	Sequence 28, Appl
31	495.5	78.2	232	2	US-07-934-373C-26	Sequence 26, Appl
32	495.5	78.2	232	3	US-08-437-642B-26	Sequence 26, Appl
33	495.5	78.2	232	5	PCT-US93-07832-26	Sequence 26, Appl
34	494.5	78.0	232	2	US-07-934-373C-38	Sequence 38, Appl
35	494.5	78.0	232	3	US-08-437-642B-38	Sequence 38, Appl
36	494.5	78.0	232	5	PCT-US93-07832-38	Sequence 38, Appl
37	493.5	77.8	232	2	US-07-934-373C-35	Sequence 35, Appl
38	493.5	77.8	232	3	US-08-437-642B-35	Sequence 35, Appl
39	493.5	77.8	232	5	PCT-US93-07832-35	Sequence 35, Appl
40	493.5	77.8	232	3	US-08-437-642B-36	Sequence 36, Appl
41	493.5	77.8	232	5	PCT-US93-07832-36	Sequence 36, Appl
42	493.5	77.8	232	2	US-07-934-373C-33	Sequence 33, Appl
43	492.5	77.7	232	2	US-08-437-642B-33	Sequence 33, Appl
44	492.5	77.7	232	5	PCT-US93-07832-33	Sequence 33, Appl
45	492.5	77.7	232	5	PCT-US93-07832-33	Sequence 33, Appl

## ALIGNMENTS

RESULT 1  
US-07-934-373C-27  
Sequence 27, Application US/07934373C  
Patent No. 5621337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

Query Match 79.4%; Score 503.5; DB 2; Length 232;  
Best Local Similarity 77.8%; Pred. No. 4.4e-42;  
Matches 98; Conservative 6; Mismatches 15; Indels 7; Gaps 1;  
CY 1 EVOLVESGGGLVQPGGSLRLSCATSGYTFEYIIHWKRAFGKGLENVASINPDYLTNY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYIMHWKQAPGKGLEWVAGINPNKGSTH 60  
QY 61 NORFKRFTSLDKSKRTAYLQNNSLRAEDTAVYYCAWSIS-----DFPDYWGQSTLV 113  
Db 61 NORFMDRFTLSVDKSKNTLYLQNNSLRAEDTAVYYCAWRGLNGYFDVRYFDVWGQSTLV 120  
QY 114 TVSSAS 119  
Db 121 TVSSAS 126

RESULT 2  
US-08-437-642B-27  
Sequence 27, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-437-642B-27

Query Match 79.4%; Score 503.5; DB 3; Length 232;  
Best Local Similarity 77.8%; Pred. No. 4.4e-42;  
Matches 98; Conservative 6; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYIMHWQAPGKGLEWVAGINPDYDITNY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYIMHWQAPGKGLEWVAGINPNKGSTH 60  
QY 61 NORFKRFTSLDKSKRTAYLQNNSLRAEDTAVYYCAWSIS-----DFPDYWGQSTLV 113

Db 61 NORFMDRFTLSVDKSKNTLYLQNNSLRAEDTAVYYCAWRGLNGYFDVRYFDVWGQSTLV 120  
QY 114 TVSSAS 119  
Db 121 TVSSAS 126

RESULT 3  
PCT-US93-07832-27  
Sequence 27, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patlin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-27

Query Match 79.4%; Score 503.5; DB 5; Length 232;  
Best Local Similarity 77.8%; Pred. No. 4.4e-42;  
Matches 98; Conservative 6; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYIMHWKQAPGKGLEWVAGINPDYDITNY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYIMHWKQAPGKGLEWVAGINPNKGSTH 60  
QY 61 NORFKRFTSLDKSKRTAYLQNNSLRAEDTAVYYCAWSIS-----DFPDYWGQSTLV 113  
Db 61 NORFMDRFTLSVDKSKNTLYLQNNSLRAEDTAVYYCAWRGLNGYFDVRYFDVWGQSTLV 120  
QY 114 TVSSAS 119  
Db 121 TVSSAS 126

RESULT 4  
US-07-934-373C-29



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-29

Query Match 78.8%; Score 499.5; DB 3; Length 232;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCATSGYTFETYYIHWRQAPGKLEWVASINPDYDITNY 60  
1 EVOLVESGGGLVOPGSLRLSCATSGYTFETYYIHWRQAPGKLEWVASINPDYDITNY 60  
DB 61 NORFKGRFTISLDKSKRTAYLQWNSLRADTAVYVCASWIS-----DFPDYWGQGLTV 113  
61 NORFKGRFTISLDKSKRTAYLQWNSLRADTAVYVCASWIS-----DFPDYWGQGLTV 120  
QY 114 TVSSAS 119  
114 TVSSAS 126  
DB 121 TVSSAS 126

RESULT 7  
PCT-US93-07832-29  
Sequence 29, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:

NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-29

Query Match 78.8%; Score 499.5; DB 5; Length 232;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCATSGYTFETYYIHWRQAPGKLEWVASINPDYDITNY 60  
1 EVOLVESGGGLVOPGSLRLSCATSGYTFETYYIHWRQAPGKLEWVASINPDYDITNY 60  
DB 61 NORFKGRFTISLDKSKRTAYLQWNSLRADTAVYVCASWIS-----DFPDYWGQGLTV 113  
61 NORFKGRFTISLDKSKRTAYLQWNSLRADTAVYVCASWIS-----DFPDYWGQGLTV 120  
QY 114 TVSSAS 119  
114 TVSSAS 126  
DB 121 TVSSAS 126

RESULT 8  
US-07-934-373C-30  
Sequence 30, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: Amino Acid

TOPOLOGY: Linear  
US-07-934-373C-30

Query Match 78.8%; Score 499.5; DB 2; Length 235;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDTNY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 120

QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 9  
US-08-437-642B-30

Sequence 30, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

US-08-437-642B-30  
Query Match 78.8%; Score 499.5; DB 3; Length 235;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;

Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDTNY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 120

QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 10  
PCT-US93-07832-30

Sequence 30, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

PCT-US93-07832-30  
Query Match 78.8%; Score 499.5; DB 5; Length 235;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDTNY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCATSGYTFEYIIHWVROAPGKLEWVASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQWNSLRAEDTAVYYCASWIS-----DFPDYWGQGLTV 120

US-08-437-642B-30  
Query Match 78.8%; Score 499.5; DB 3; Length 235;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;



ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpacin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/460,587  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097,309  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-460-587-1

Query Match 78.8%; Score 499.5; DB 3; Length 241;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSSLRISCATSGYTFETIHHWRQAPGKLEWVASINPDYDITNY 60  
DB 1 EVOLVESGGGLVOPGSSLRISCATSGYTFETIHHWRQAPGKLEWVASINPDYDITNY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLQMNLSRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NQRFMDRFTISVDKSTSTAYLQMNLSRAEDTAVYYCARMRGIANGFVRYFDVWGQGLTV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 14  
US-09-940-166A-1  
Sequence 1, Application US/09940166A  
Patent No. 6716598  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpacin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,166A  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097,309  
FILING DATE: 13-JUN-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-940-166A-1

Query Match 78.8%; Score 499.5; DB 4; Length 241;  
Best Local Similarity 77.0%; Pred. No. 1.1e-41;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSSLRISCATSGYTFETIHHWRQAPGKLEWVASINPDYDITNY 60  
DB 1 EVOLVESGGGLVOPGSSLRISCATSGYTFETIHHWRQAPGKLEWVASINPDYDITNY 60  
QY 61 NQRFKGRFTISLDKSKRTAYLQMNLSRAEDTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NQRFMDRFTISVDKSTSTAYLQMNLSRAEDTAVYYCARMRGIANGFVRYFDVWGQGLTV 120  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126

RESULT 15  
US-09-097-309-7  
Sequence 7, Application US/09097309  
Patent No. 6121428  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpacin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/097,309  
FILING DATE: 12-Jun-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050951  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

US-09-097-309-7

Query Match 78.8%; Score 499.5; DB 3; Length 300;  
 Best Local Similarity 77.0%; Pred. No. 1.5e-41;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAATSGYTFTEYIIHWVRQAPEGKLEWVASINPDYDITNY 60  
 |||||  
 Db 24 EVQLVESGGGLVQPGGSLRLSCAATSGYTFTEYTHMMWRQAPGKLEWVAGINPNGGTSH 83  
 |||||  
 QY 61 NORPKGRFTISLDKSKRTAYLQMSLRAEDTAVYYCASWIS-----DPDYWGQGTLY 113  
 |||||  
 Db 84 NORPMDFRTISVDKSTISTAYQMNSLRAEDTAVYYCARWRGLNYGPDVRYFDVWGQGTLY 143  
 |||||  
 QY 114 TVSSAS 119  
 |||||  
 Db 144 TVSSAS 149

Search completed: December 29, 2004, 19:37:37  
 Job time : 29.6009 secs



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OM protein - protein search, using BW model

Run on: December 29, 2004, 18:59:15 ; Search time 122.575 Seconds  
(without alignments)  
348.266 Million cell updates/sec

Title: US-10-044-896-5

Perfect score: 634  
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....ISDFPDYWGQGTITVSSAS 119

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*\n2: Geneseqp1990s:\*\n3: Geneseqp2000s:\*\n4: Geneseqp2001s:\*\n5: Geneseqp2002s:\*\n6: Geneseqp2003as:\*\n7: Geneseqp2003bs:\*\n8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	634	100.0	119	5	AAE28150 Humanised
2	499.5	78.8	232	2	AAW34503 Heavy cha
3	499.5	78.8	232	2	AAV08753 Human ant
4	499.5	78.8	232	5	ABG31888 Humanised
5	499.5	78.8	232	8	ADK18341 Amino aci
6	499.5	78.8	241	2	AAW95614 Humanized
7	499.5	78.8	241	4	AAE66776 rhuMab CD
8	499.5	78.8	277	2	AAW30631 Recombina
9	499.5	78.8	300	2	AAW95623 pS1130 ex
10	499.5	78.8	300	2	AAW30635 Recombina
11	499.5	78.8	300	4	AAE66785 Proteina
12	499.5	78.8	300	6	ABP72746 Anti-CD18
13	499.5	78.8	450	2	AAW34505 Heavy cha
14	499.5	78.8	450	2	AAV08755 Human Igg
15	499.5	78.8	450	5	ABG31890 Full leng
16	499.5	78.8	450	8	ADK18343 Amino aci
17	499.5	78.8	537	3	AAE03664 Anti-CD18
18	499.5	78.8	552	3	AAE30775 pHS2-8.0
19	493	77.8	119	5	AAE28147 Murine 9F
20	487	76.8	119	4	AAE62086 Humanised
21	487	76.8	119	4	AAE60399 Humanised
22	487	76.8	119	4	AAE61584 Humanised
23	487	76.8	119	5	AAU74540 Human ant
24	487	76.8	119	8	ADK18343 Humanise
25	487	76.8	119	8	ADJ88007 Humanised

26	487	76.8	119	8	ADN12053 Variable
27	487	76.8	119	8	ADP43327 Humanised
28	481	75.9	451	8	ADFI1670 anti-CD11
29	480.5	75.8	122	2	AAE30772 huCD3v9,
30	477.5	75.3	253	2	AAV29444 Humanised
31	477.5	75.3	253	2	AAV29454 Humanised
32	477.5	75.3	253	3	AAV77757 Humanised
33	477.5	75.3	253	3	AAV77759 Humanised
34	477.5	75.3	253	3	AAE30316 6G4-2-5V1
35	477.5	75.3	253	3	AAE30314 Humanised
36	477.5	75.3	253	6	ABU13791 Humanised
37	477.5	75.3	253	6	ABU13793 Humanised
38	477.5	75.3	253	6	ABU59506 Humanised
39	477.5	75.3	253	6	ABU59504 Humanised
40	477.5	75.3	253	7	AAE39089 Humanised
41	477.5	75.3	253	7	AAE39086 Humanised
42	477.5	75.3	256	2	AAE63304 Humanised
43	477.5	75.3	256	2	AAV29457 6G4V1N35
44	477.5	75.3	256	3	AAV77765 Humanised
45	477.5	75.3	256	3	AAE30321 Humanised

#### ALIGNMENTS

RESULT 1	
ID	AAE28150
XX	AAE28150 standard; protein; 119 AA.
XX	
AC	AAE28150;
XX	
DT	27-DEC-2002 (first entry)
XX	
DE	Humanised 9F3 version 13 (V13) heavy chain variable domain.
XX	
KW	Human; interferon alpha; IFNalpha; insulin-dependent diabetes mellitus;
KW	autoimmune disease; systemic lupus erythematosus; autoimmune thyroiditis;
KW	antibody therapy; immunosuppressive; antiinflammatory; dermatological;
KW	9F3 monoclonal antibody; heavy chain variable domain.
XX	
OS	Homo sapiens.
OS	Synthetic.
PH	
FT	Key
FT	Location/Qualifiers
FT	26..35
FT	/note= "Complementarity determining region 1 (CDR1)"
FT	50..66
FT	/note= "Complementarity determining region 2 (CDR2)"
FT	99..106
FT	/note= "Complementarity determining region 3 (CDR3)"
XX	
PE	29-JAN-2002; 2002WO-US002709.
XX	
PR	22-FEB-2001; 2001US-0270775P.
PR	09-JAN-2002; 2002US-00044896.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Chuntarapai A, Kim JK, Presta LG, Stewart T;
XX	
DR	WPI; 2002-682767/73.
XX	
PT	New anti-interferon alpha monoclonal antibody, 9F3, useful for treating
PT	autoimmune diseases e.g. insulin-dependent diabetes mellitus, systemic
PT	lupus erythematosus and autoimmune thyroiditis.
XX	
PS	Disclosure; Page 98; 100p; English.
XX	
CC	The present invention relates to novel anti-interferon alpha (IFNalpha)

CC monoclonal antibody, 9F3 which binds to and neutralises a biological  
CC activity of IFN-alpha subtypes. The anti-IFNalpha monoclonal antibodies  
CC of the invention are useful for treating autoimmune diseases such as  
CC insulin-dependent diabetes mellitus, systemic lupus erythematosus and  
CC autoimmune thyroiditis. They are useful as reagents in diagnostic assays  
CC for IFN-alpha expression, for the affinity purification of various IFN-  
CC alpha subtypes from recombinant cell culture or natural resources and for  
CC the detection of IFN-alpha in diagnostic assay methods. Sequences of the  
CC invention are also useful in antibody therapy. The present sequence is  
CC anti-human IFNalpha monoclonal antibody 9F3 version 13 (V13) heavy chain  
CC variable domain  
CC  
XX  
SQ Sequence 119 AA;  
  
Query Match 100.0%; Score 634; DB 5; Length 119;  
Best Local Similarity 100.0%; Pred. No. 4.1e-52;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EVQLVESGGGLVQPGGSLRLSCATGTYFTFYIIMHWROAPGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCATGTYFTFYIIMHWROAPGKLEWVASINPDYDITNY 60  
  
QY 61 NORFKGRFTISLDKSKRTAYLQNMNSLRADTAVYYCASWISDFPDYWGQGLTVVSSAS 119  
DB 61 NORFKGRFTISLDKSKRTAYLQNMNSLRADTAVYYCASWISDFPDYWGQGLTVVSSAS 119  
  
RESULT 2  
AAW34503  
ID AAW34503 standard; protein; 232 AA.  
XX  
AC AAW34503;  
XX  
DT 19-MAR-1998 (first entry)  
XX  
DE Heavy chain of humanised H52 antibody.  
XX  
KM Humanised antibody; HuH52; heavy chain; focal ischaemic stroke; embolism;  
KM brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;  
KM transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;  
KM systemic hypoperfusion; cardiac arrest.  
XX  
OS Synthetic.  
OS Homo sapiens.  
OS Mus sp.  
XX  
FN W09726912-A2.  
XX  
PD 31-JUL-1997.  
XX  
PF 11-JAN-1997; 97WO-US000492.  
XX  
PR 23-JAN-1996; 96US-00589982.  
XX  
PA (GETH ) GENENTECH INC.  
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
XX  
PI Bednar MM, Gross CE, Thomas GR;  
XX  
DR WPI; 1997-393373/36.  
XX  
PT Administering an anti-CD18 antibody to treat focal ischaemic stroke - by  
PT increasing cerebral blood flow and reducing size of brain infarct.  
XX  
PS Disclosure; Page 9; 41pp; English.  
XX  
CC This sequence represents the heavy chain of the humanised H52 antibody.  
CC The H52 antibody can be used in the method of the invention. The method  
CC is for treating focal ischaemic stroke, i.e. damage to the brain due to  
CC interrupted blood supply, in a mammal, caused by obstruction of a main  
CC cerebral artery, comprises administering anti-CD18 antibody to increase  
CC cerebral blood flow and/or reduce the size of the area of brain that  
CC dies, without removing the arterial obstruction. CD18, is upregulated in

CC patients after ischaemic stroke or transient ischaemic attack (stroke  
CC symptoms last less than 24 hours with complete recovery). Treatment with  
CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain  
CC infarct size, improving clinical outcomes in focal ischaemic strokes in  
CC mammals, particularly in humans. The method provides an alternative to  
CC thrombolytic therapy for treating ischaemic strokes caused by  
CC thromboembolism (thrombosis or embolism), particularly where thrombolytic  
CC therapy has been unsuccessful, is contra-indicated e.g. because such  
CC drugs exacerbate bleeding, or is unsuitable because of the time delay  
CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue  
CC plasminogen activator) may also be administered before, after or  
CC simultaneously with the anti-CD18 antibody. Alternatively, the method can  
CC be used to treat the third main type of ischaemic stroke, systemic  
CC hypoperfusion, e.g. resulting from cardiac arrest or drowning  
XX  
SQ Sequence 232 AA;  
  
Query Match 78.8%; Score 499.5; DB 2; Length 232;  
Best Local Similarity 77.0%; Pred. No. 4.2e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
  
QY 1 EVQLVESGGGLVQPGGSLRLSCATGTYFTFYIIMHWROAPGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCATGTYFTFYIMHWROAPGKLEWVASINPDYDITNY 60  
  
QY 61 NORFKGRFTISLDKSKRTAYLQNMNSLRADTAVYYCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORFKGRFTISLDKSKRTAYLQNMNSLRADTAVYYCASWISDFPDYWGQGLTV 120  
  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
  
RESULT 3  
AAV08753  
ID AAV08753 standard; protein; 232 AA.  
XX  
AC AAV08753;  
XX  
DT 10-AUG-1999 (first entry)  
XX  
DE Human antibody huH52 heavy chain protein fragment.  
XX  
KM IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;  
KM IgG4; kappa-C1 domain; lambda-C1 domain; focal ischaemic stroke;  
KM cerebroprotective; cerebral artery obstruction; blood flow; infarct;  
KM CD18 extracellular domain; endothelium; CD1b/CD18 complex dissociation;  
KM antibody; huH52; heavy chain.  
XX  
OS Homo sapiens.  
XX  
FN US5914112-A.  
XX  
PD 22-JUN-1999.  
XX  
PF 22-JAN-1997; 97US-00788800.  
XX  
PR 23-JAN-1996; 96US-0093038P.  
XX  
PA (GETH ) GENENTECH INC.  
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
XX  
PI Thomas GR, Bednar MM, Gross CE;  
XX  
DR WPI; 1999-370483/31.  
XX  
PT Anti-CD18 antibodies in stroke.  
XX  
PS Claim 11; Col 29-32; 25pp; English.  
XX  
CC This invention describes a method for improving the clinical outcome in  
CC focal ischaemic stroke by administering novel anti-CD18 antibody which

CC has cerebroprotective properties. The invention particularly describes a  
CC method of treating focal ischaemic stroke caused by the obstruction of a  
CC main cerebral artery which comprises administering an anti-CD18 antibody  
CC to increase the blood flow or reduce the infarct size, where: (1) the  
CC antibody binds to an extracellular domain of CD18 and inhibits or reduces  
CC the ability of the cell expressing CD18 to bind to endothelium, (2) the  
CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the  
CC antibody dissociates CD18/CD18 complex. This sequence represents the  
CC human antibody huH52 heavy chain region  
XX  
SQ Sequence 232 AA;  
Query Match 78.8%; Score 499.5; DB 2; Length 232;  
Best Local Similarity 77.0%; Pred. No. 4.2e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
QY 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFTEYIIHWROAPRGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFTEYIIHWROAPRGKLEWVASINPDYDITNY 60  
QY 61 NORPKGRFTISLDKSKRTAYLQNMNSLRADPTAVYTCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORPKGRFTISLDKSKRTAYLQNMNSLRADPTAVYTCASWIS-----DFPDYWGQGLTV 113  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
Db 121 TVSSAS 126  
RESULT 4  
ABG31888  
ID ABG31888 standard; peptide; 232 AA.  
XX  
AC ABG31888;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Humanised H52 antibody (huH52) Fab fragment, heavy chain.  
XX  
KW Human; humanised H52 antibody; huH52; cerebral blood flow; infarct size;  
KW focal ischaemic stroke; main cerebral artery;  
KW tissue plasminogen activator; anti-CD18 antibody; stroke;  
KW acute ischaemic stroke; thrombolytic therapy;  
KW FcγRIb surface receptor binding epitope; thromboembolic stroke.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US2002081294-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 20-DEC-2000; 2000US-00811384.  
XX  
PR 23-JAN-1996; 96US-0093038P.  
PR 22-JAN-1997; 97US-00788800.  
PR 17-FEB-1999; 99US-00251652.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bednar MM, Gross CE, Thomas GR, Gross LJ;  
XX  
DR WPI; 2004-626528/67.  
XX  
PT Increasing cerebral blood flow and/or reducing infarct size in focal  
PT ischemic stroke using anti-CD18 antibody and tissue plasminogen activator  
PT is useful to improve clinical outcome in acute ischemic stroke.  
XX  
PS Claim 11; Page 5; 27pp; English.  
XX  
CC The invention relates to a method of increasing cerebral blood flow and/  
CC or reducing infarct size in focal ischaemic stroke caused by obstruction  
CC of a main cerebral artery in a human, comprising co-administering tissue

CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the  
CC stroke. The method is used to improve the clinical outcome in acute  
CC ischaemic stroke and to provide an alternative to thrombolytic therapy  
CC for treating thromboembolic stroke, particularly where thrombolytic  
CC therapy has been unsuccessful or is contra-indicated. The present  
CC sequence represents a humanised H52 antibody (huH52) Fab, heavy chain  
CC used in the method of the invention  
XX  
SQ Sequence 232 AA;  
Query Match 78.8%; Score 499.5; DB 5; Length 232;  
Best Local Similarity 77.0%; Pred. No. 4.2e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;  
QY 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFTEYIIHWROAPRGKLEWVASINPDYDITNY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCLATSGYTFTEYIIHWROAPRGKLEWVASINPDYDITNY 60  
QY 61 NORPKGRFTISLDKSKRTAYLQNMNSLRADPTAVYTCASWIS-----DFPDYWGQGLTV 113  
DB 61 NORPKGRFTISLDKSKRTAYLQNMNSLRADPTAVYTCASWIS-----DFPDYWGQGLTV 113  
QY 114 TVSSAS 119  
DB 121 TVSSAS 126  
Db 121 TVSSAS 126  
RESULT 5  
ADK18341  
ID ADK18341 standard; protein; 232 AA.  
XX  
AC ADK18341;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Amino acid sequence of humanised H52 (huH52) Fab heavy chain.  
XX  
KW Cerebral blood flow; infarct size; focal ischaemic stroke;  
KW cerebral artery; tissue plasminogen activator; tPA; anti-CD18 antibody;  
KW humanised H52 antibody; huH52 Fab; stroke; cerebroprotective; vasotropic;  
KW human; heavy chain.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US2004057951-A1.  
XX  
PD 25-MAR-2004.  
XX  
PF 31-MAR-2003; 2003US-00404286.  
XX  
PR 23-JAN-1996; 96US-0093038P.  
PR 22-JAN-1997; 97US-00788800.  
PR 17-FEB-1999; 99US-00251652.  
PR 20-DEC-2000; 2000US-00811384.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bednar MM, Gross CE, Thomas GR, Gross LJ;  
XX  
DR WPI; 2004-257111/24.  
XX  
PT Increasing cerebral blood flow and/or reducing infarct size in focal  
PT ischemic stroke caused by obstruction of a main cerebral artery in a  
PT human comprises co-administering tissue plasminogen activator and anti-  
PT CD18 antibody.  
XX  
PS Claim 11; SEQ ID NO 10; 26pp; English.  
XX  
CC The present invention relates to a method for increasing cerebral blood  
CC flow and/or reducing infarct size in focal ischaemic stroke caused by  
CC obstruction of a main cerebral artery in a mammal, particularly humans.  
CC The method comprises co-administering tissue plasminogen activator (tPA)

CC and anti-CD18 antibody to the mammal, where neither the tPA nor the anti-  
CC CD18 antibody is administered to the mammal until about 3-5 hours after  
CC the onset of focal ischaemic stroke. The anti-CD18 antibody is a  
CC humanised H52 antibody (huH52 Fab). The anti-CD18 antibody binds to an  
CC extracellular domain of CD18 and inhibits or reduces the ability of a  
CC cell expressing CD18 to bind to endothelium. The anti-CD18 antibody binds  
CC CD18 with an affinity of 1-4 nm or less. The anti-CD18 antibody  
CC dissociates the CD11b/CD18 complex. The anti-CD18 antibody binds to the  
CC epitope bound by H52 antibody. The anti-CD18 antibody and the tPA are  
CC simultaneously administered to the mammal, or the anti-CD18 antibody is  
CC administered before the tPA is administered to the mammal. The method is  
CC useful in increasing cerebral blood flow and/or reducing infarct size in  
CC focal ischaemic stroke caused by obstruction of a main cerebral artery in  
CC a human. The antibodies are particularly useful for treating stroke.  
CC Unlike previous methods, the new method of treatment does not require  
CC prior administration of a thrombolytic agent to the mammal in order to  
CC remove an embolus/thrombus, and therefore increases cerebral blood flow  
CC and/or reduces infarct size. The present sequence represents the heavy  
CC chain of huH52 Fab.

SQ Sequence 232 AA;

Query Match 78.8%; Score 499.5; DB 8; Length 232;

Best Local Similarity 77.0%; Pred. No. 4.2e-39;

Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLRLSCATSGYTFEYTHHWROAPGKGLBWAASINPDYDTNY 60

DB 1 EVQLVESGGGLVPGGSLRLSCATSGYTFEYTHHWROAPGKGLBWAASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSRRTAYLQNNSLRAEDTAVYVCASWIS-----DFDYWGQGLTV 113

DB 61 NORFKGRFTISLDKSRRTAYLQNNSLRAEDTAVYVCASWIS-----DFDYWGQGLTV 120

QY 114 TVSSAS 119

DB 121 TVSSAS 126

## RESULT 6

ID AAM95614 standard; protein; 241 AA.

XX AAM95614;

DT 08-JUN-1999 (first entry)

XX Humanized anti-CD18 antibody rhumAb CD18 heavy chain.

KM Monoclonal antibody; heavy chain; humanized; myocardial infarction;

KW burns; thermal injury; ischemic; shock; ischaemic; haemorrhagic;

XX Mus musculus.

XX Synthetic.

XX WO9856418-A1.

PD 17-DEC-1998.

PF 12-JUN-1998; 98WO-US0122209.

PR 13-JUN-1997; 97US-00874897.

PA (GETH ) GENENTECH INC.

PI Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z, Wang SX;

XX Weisburg RP, Wong RU,

XX WPI; 1999-080860/07.

PT New stable aqueous antibody formulations - comprising an antibody not  
PT subjected to lyophilisation, a buffer maintaining the pH at 4.5 - 6, a

PT surfactant and a polyol.

PS Disclosure; Fig 1A; 87pp; English.

CC The sequence is that of the heavy chain of a humanized murine anti-CD18  
CC antibody rhumAb CD18. It can be used for the treatment of disorders which  
CC include haemorrhagic shock, thermal injury (such as that resulting from  
CC burns), stroke (including ischaemic and haemorrhagic stroke) and  
CC myocardial infarction. The antibody formulation can be stabilised at 30  
CC temperature of 2-8 deg. C for at least one year or at a temperature of 30  
CC deg. C for at least one month and is stable following freezing and  
CC thawing

SQ Sequence 241 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 241;

Best Local Similarity 77.0%; Pred. No. 4.4e-39;

Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLRLSCATSGYTFEYTHHWROAPGKGLBWAASINPDYDTNY 60

DB 1 EVQLVESGGGLVPGGSLRLSCATSGYTFEYTHHWROAPGKGLBWAASINPDYDTNY 60

QY 61 NORFKGRFTISLDKSRRTAYLQNNSLRAEDTAVYVCASWIS-----DFDYWGQGLTV 113

DB 61 NORFKGRFTISLDKSRRTAYLQNNSLRAEDTAVYVCASWIS-----DFDYWGQGLTV 120

QY 114 TVSSAS 119

DB 121 TVSSAS 126

## RESULT 7

ID AAB66776 standard; protein; 241 AA.

XX AAB66776;

DT 10-APR-2001 (first entry)

XX rhumAb CD18 heavy chain.

KM Antibody; lyophilization; hemorrhagic shock; thermal injury;

KW myocardial infarction; inflammation.

XX Homo sapiens.

XX US6171586-B1.

PD 09-JAN-2001.

PF 12-JUN-1998; 98US-00097171.

PR 13-JUN-1997; 97US-0053087P.

PA (GETH ) GENENTECH INC.

PI Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z, Wang SX;

XX Weisburg RP, Wong RU,

XX WPI; 2001-136863/14.

PT Stable aqueous pharmaceutical formulation for treating hemorrhagic shock,  
PT thermal injury, stroke, and myocardial infarction, comprises an antibody  
PT not subjected to prior lyophilization.

PS Example 1; Fig 1; 56pp; English.

CC The present invention relates to a stable aqueous pharmaceutical  
CC formulation, comprising an antibody not subjected to prior  
CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and a  
CC polyol. The invention is useful for treating hemorrhagic shock, thermal  
CC injury, e.g. resulting from burns, stroke including ischemic and

CC hemorrhagic stroke, myocardial infarction, inflammatory disorders such as  
 CC adult respiratory distress syndrome (ARDS), hypovolemic shock, ulcerative  
 CC colitis, rheumatoid arthritis and B-cell lymphomas  
 XX

Sequence 241 AA;

Query Match 78.8%; Score 499.5; DB 4; Length 241;  
 Best Local Similarity 77.0%; Pred. No. 4,4e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSGRLSCATSGYTFETYYIHVWQAPKGLWVASINPDYDITNY 60  
 DB 1 EVOLVESGGGLVQPGSGRLSCATSGYTFETYYIHVWQAPKGLWVASINPDYDITNY 60  
 QY 61 NORPKGRTTISLDKSKRTAYLQMNSLRAEDTAVVYVCASWIS-----DFPDYWGQGLTV 113  
 DB 61 NORPKGRTTISLDKSKRTAYLQMNSLRAEDTAVVYVCASWIS-----DFPDYWGQGLTV 120  
 QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

RESULT 8  
 AAW30631  
 ID AAW30631 standard; protein; 277 AA.

AAW30631;  
 06-APR-1999 (first entry)

Recombinant humanised anti-CD18 antibody rhumab CD18 heavy chain.

Recombinant humanised anti-CD18 antibody; rhumab CD18; leucine zipper;  
 murine monoclonal antibody; mUMAB H52; protein recovery; filtration;  
 chromatography.

Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 Region 242..277  
 /label= leucine\_zipper

WO9856808-A1.

17-DEC-1998.

12-JUN-1998; 98WO-US012334.

13-JUN-1997; 97US-0050951P.

(GERTH ) GENENTECH INC.

Blank GS, Narindray DS, Zapata GA;

WPI; 1999-060267/05.

New method for recovering polypeptides from cell cultures - by treating  
 with reagent and filtering to remove reagent.

Example; Fig 1A; 43pp; English.

A method has been developed for recovering a polypeptide comprising: (a)  
 exposing a composition comprising a polypeptide to a reagent which binds  
 to or modifies the polypeptide, where the reagent is immobilized on a  
 solid phase; and (b) passing the composition through a filter bearing an  
 opposite charge to the reagent so as to remove leached reagent from the  
 composition. The present invention also describes a method for modifying  
 a precursor antibody comprising a leucine zipper by exposing the  
 precursor antibody to a protease immobilized on a solid support so that  
 the protease removes the zipper. The method can be used to purify

CC proteins from cell cultures. They are especially useful for isolating  
 CC antibodies. The methods overcome the problem of reagent leakage into the  
 CC protein as is the case in prior art immobilized modification systems. By  
 CC using a opposite charge filter the reagent can be excluded from the  
 CC sample, preventing contamination. The present sequence represents the  
 CC recombinant humanised anti-CD18 antibody (rhumab CD18) heavy chain, which  
 CC is used in an example from the present invention

Sequence 277 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 277;  
 Best Local Similarity 77.0%; Pred. No. 5.1e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSGRLSCATSGYTFETYYIHVWQAPKGLWVASINPDYDITNY 60  
 DB 1 EVOLVESGGGLVQPGSGRLSCATSGYTFETYYIHVWQAPKGLWVASINPDYDITNY 60  
 QY 61 NORPKGRTTISLDKSKRTAYLQMNSLRAEDTAVVYVCASWIS-----DFPDYWGQGLTV 113  
 DB 61 NORPKGRTTISLDKSKRTAYLQMNSLRAEDTAVVYVCASWIS-----DFPDYWGQGLTV 120  
 QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

RESULT 9  
 AAW95623  
 ID AAW95623 standard; protein; 300 AA.

AAW95623;  
 08-JUN-1999 (first entry)

PS1130 expression cassette encoded rhumab CD18 heavy chain.

Monoclonal antibody; heavy chain; humanized; myocardial infarction;  
 burns; thermal injury; ischemic; shock; ischaemic; haemorrhagic;  
 hemorrhagic; stroke; heavy chain.

Mus musculus.  
 OS Synthetic.

Key Location/Qualifiers  
 Peptide 1..23

WO9856418-A1.

17-DEC-1998.

12-JUN-1998; 98WO-US012209.

13-JUN-1997; 97US-00874897.

(GERTH ) GENENTECH INC.

Lam XM, Oeswein JQ, Ongpipatanakul B, Shahrokh Z, Wang SX;

WPI; 1999-080860/07.

New stable aqueous antibody formulations - comprising an antibody not  
 subjected to lyophilisation, a buffer maintaining the pH at 4.5 - 6, a  
 surfactant and a polyol.

Disclosure; Fig 21A; 87pp; English.

The sequence is that of the PS1130 encoded heavy chain of a humanized  
 CC murine anti-CD18 antibody rhumab CD18. It can be used for the treatment of  
 CC disorders which include haemorrhagic shock, thermal injury (such as that  
 CC resulting from burns), stroke (including ischaemic and haemorrhagic  
 CC stroke) and myocardial infarction. The antibody formulation can be

CC stabilised at a temperature of 2-8 deg. C for at least one year or at a  
CC temperature of 30 deg. C for at least one month and is stable following  
CC freezing and thawing  
XX

SO Sequence 300 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 300;  
Best Local Similarity 77.0%; Pred. No. 5.5e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATGYPTEYIIHWMRQAPGKLEWVASINPDYDTNY 60

DB 24 EVOLVESGGGLVPGGSLRLSCATGYPTEYIIHWMRQAPGKLEWVASINPDYDTNY 83

QY 61 NORFKGRFTISLDKSKRTAYLQNNSLRAEDTAVYYCASWIS-----DFPDYWGQGLV 113

DB 84 NORFKGRFTISLDKSKRTAYLQNNSLRAEDTAVYYCASWIS-----DFPDYWGQGLV 143

QY 114 TVSSAS 119

DB 144 TVSSAS 149

RESULT 10

AAM30635  
ID AAM30635 standard; protein; 300 AA.

AC AAM30635;

DT 06-APR-1999 (first entry)

XX Recombinant humanised anti-CD18 antibody rhumab CD18 heavy chain.

KM Recombinant humanised anti-CD18 antibody; rhumab CD18; leucine zipper;

KW murine monoclonal antibody; mumb H52; protein recovery; filtration;

XX chromatography.

OS Mus sp.

OS Homo sapiens.

OS Synthetic.

XX

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XX

XX

Example; Fig 4; 43pp; English.

A method has been developed for recovering a polypeptide comprising: (a)

exposing a composition comprising a polypeptide to a reagent which binds

to or modifies the polypeptide, where the reagent is immobilized on a

solid phase; and (b) passing the composition through a filter bearing an

opposite charge to the reagent so as to remove leached reagent from the

composition. The present invention also describes a method for modifying

a precursor antibody comprising a leucine zipper by exposing the

CC the protease removes the zipper. The methods can be used to purify  
CC proteins from cell cultures. They are especially useful for isolating  
CC antibodies. The methods overcome the problem of reagent leakage into the  
CC protein as is the case in prior art immobilized modification systems. By  
CC using a opposite charge filter the reagent can be excluded from the  
CC sample, preventing contamination. The present sequence represents the  
CC recombinant humanised anti-CD18 antibody (rhumb CD18) heavy chain, which  
CC is used in an example from the present invention  
XX

SO Sequence 300 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 300;  
Best Local Similarity 77.0%; Pred. No. 5.5e-39;  
Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVPGGSLRLSCATGYPTEYIIHWMRQAPGKLEWVASINPDYDTNY 60

DB 24 EVOLVESGGGLVPGGSLRLSCATGYPTEYIIHWMRQAPGKLEWVASINPDYDTNY 83

QY 61 NORFKGRFTISLDKSKRTAYLQNNSLRAEDTAVYYCASWIS-----DFPDYWGQGLV 113

DB 84 NORFKGRFTISLDKSKRTAYLQNNSLRAEDTAVYYCASWIS-----DFPDYWGQGLV 143

QY 114 TVSSAS 119

DB 144 TVSSAS 149

RESULT 11

AAB6785  
ID AAB6785 standard; protein; 300 AA.

AC AAB6785;

DT 10-APR-2001 (first entry)

XX Protein encoded by ps 1130 expression cassette.

KM Antibody; lyophilization; hemorrhagic shock; thermal injury;

KW myocardial infarction; inflammation.

XX Homo sapiens.

XX US6171586-B1.

XX 09-JAN-2001.

XX 12-JUN-1998; 98US-00097171.

XX 13-JUN-1997; 97US-0053087P.

XX (GETH ) GENENTECH INC.

XX Lam XM, Oeswein JO, Ongpipattanakul B, Shahrokh Z, Wang SX;

XX Weisburg RP, Wong RL;

XX WPI; 2001-136863/14.

XX Stable aqueous pharmaceutical formulation for treating hemorrhagic shock,

XX thermal injury, stroke, and myocardial infarction, comprises an antibody

XX not subjected to prior lyophilization.

XX Disclosure; Fig 21; 56pp; English.

The present invention relates to a stable aqueous pharmaceutical

formulation, comprising an antibody not subjected to prior

lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and a

polysol. The invention is useful for treating hemorrhagic shock, thermal

SQ Sequence 300 AA;

Query Match 78.8%; Score 499.5; DB 4; Length 300;  
 Best Local Similarity 77.0%; Pred. No. 5.5e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETIIMHWQAQPKGLEWVASINPDYDITNY 60  
 DB 24 EVQLVESGGGLVQPGGSLRLSCATSGYTFETIIMHWQAQPKGLEWVASINPDYDITNY 83

QY 61 NQRFKGRFTISLDKSKRTAYLQWNSLRADTAIVYTCASWIS-----DFPDYWGQGLTV 113  
 DB 84 NQRFMDRFTISVDKSTSTAYVQWNSLRADTAIVYTCARWRGLNYGPDVRYPDVWGQGLTV 143

QY 114 TVSSNS 119  
 DB 144 TVSSNS 149

RESULT 12

ID ABP72746 standard; protein; 300 AA.  
 AC ABP72746;  
 XX 11-JUN-2003 (first entry)  
 DE Anti-CD18 antibody heavy chain-leucine zipper.  
 XX CD18; antibody; heavy chain; pxCd18-7T3; immunosuppressive.  
 OS Unidentified.  
 OS Escherichia coli.  
 OS Chimeric.

Key Location/Qualifiers  
 1..23  
 FT Peptide /label= Signal peptide  
 FT /note= "heat stable enterotoxin II (STII) signal"  
 FT 24..300  
 FT Protein /note= "Heavy chain-leucine zipper"  
 PN WO2003018771-A2.  
 PD 06-MAR-2003.  
 PF 26-AUG-2002; 2002WO-US027220.  
 XX 27-AUG-2001; 2001US-0315209P.  
 PA (GETH ) GENENTECH INC.  
 PI Andersen DC, Simmone LC,  
 DR WPI, 2003-278654/27.  
 DR N-PSDB; AB282071.  
 PT Producing an antibody for treating cancer or autoimmune diseases by  
 PT culturing a host cell under suitable conditions so that the light chain  
 PT and heavy chain are expressed in a sequential fashion.  
 PS Claim 52; Fig 3; 73pp; English.

The present sequence is that of an anti-CD18 antibody heavy chain including a heat stable enterotoxin II (STII) secretion signal and a C-terminal leucine zipper domain. This recombinant heavy chain is produced by host cells transformed with claimed vector pxCd18-7T3 (see AB282071). The plasmid contains 2 translational units that temporally separate the transcription of the light chain (see ABP72745) and heavy chains. Expression of the light chain is under the control of the phoA promoter, while expression of the heavy chain is under the control of the inducible Tac1 promoter. In an example from the invention, Escherichia coli 59A7 was transformed with pxCd18-7T3. The light chain was expressed initially

CC and secreted into the periplasmic space. Heavy chain production was then  
 CC induced by addition of IPTG, and F(ab')<sub>2</sub> assembly occurred almost  
 CC immediately. A yield of 4.6 +/- 0.5 g/l assembled F(ab')<sub>2</sub> was obtained, a  
 CC nearly 2-fold increase on the yield obtained using a single promoter  
 CC system. This is an example of the process of the invention for production  
 CC of recombinant antibodies in a host cell system, with temporally  
 CC separated expression of the light and heavy chains. Properly assembled,  
 CC soluble and functional antibodies (or their fragments) can be produced in  
 CC high yields for diagnostic or therapeutic applications, including  
 CC treatment of cancer or autoimmune diseases

SQ Sequence 300 AA;

Query Match 78.8%; Score 499.5; DB 6; Length 300;  
 Best Local Similarity 77.0%; Pred. No. 5.5e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETIIMHWQAQPKGLEWVASINPDYDITNY 60  
 DB 24 EVQLVESGGGLVQPGGSLRLSCATSGYTFETIIMHWQAQPKGLEWVASINPDYDITNY 83

QY 61 NQRFKGRFTISLDKSKRTAYLQWNSLRADTAIVYTCASWIS-----DFPDYWGQGLTV 113  
 DB 84 NQRFMDRFTISVDKSTSTAYVQWNSLRADTAIVYTCARWRGLNYGPDVRYPDVWGQGLTV 143

QY 114 TVSSNS 119  
 DB 144 TVSSNS 149

RESULT 13

ID AAW34505 standard; protein; 450 AA.  
 AC AAW34505;  
 XX 19-MAR-1998 (first entry)  
 DE Heavy chain of full length IgG2 humanised H52 antibody.  
 XX Humanised antibody; Huh52; heavy chain; focal ischaemic stroke; embolism;  
 KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;  
 KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;  
 KW systemic hypoperfusion; cardiac arrest.  
 XX Synthetic.  
 OS Homo sapiens.  
 OS Mus sp.  
 PN WO9726912-A2.  
 PD 31-JUL-1997.  
 PF 11-JAN-1997; 97WO-US000492.  
 XX 23-JAN-1996; 96US-00589982.  
 PA (GETH ) GENENTECH INC.  
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 PI Bednar MM, Grose CE, Thomas GR;  
 DR WPI, 1997-393373/36.  
 DR Administering an anti-CD18 antibody to treat focal ischaemic stroke - by  
 PT increasing cerebral blood flow and reducing size of brain infarct.  
 PS Disclosure; Page 9; 41pp; English.

This sequence represents the heavy chain of the humanised H52 antibody. The H52 antibody can be used in the method of the invention. The method is for treating focal ischaemic stroke, i.e. damage to the brain due to interrupted blood supply, in a mammal, caused by obstruction of a main

CC cerebral artery, comprises administering anti-CD18 antibody to increase  
 CC cerebral blood flow and/or reduce the size of the area of brain that  
 CC dies, without removing the arterial obstruction. CD18, is upregulated in  
 CC patients after ischemic stroke or transient ischemic attack (stroke  
 CC symptoms last less than 24 hours with complete recovery). Treatment with  
 CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain  
 CC infarct size, improving clinical outcomes in focal ischemic strokes in  
 CC mammals, particularly in humans. The method provides an alternative to  
 CC thrombolytic therapy for treating ischemic strokes caused by  
 CC thromboembolism (thrombosis or embolism), particularly where thrombolytic  
 CC therapy has been unsuccessful, is contra-indicated e.g. because such  
 CC drugs exacerbate bleeding, or is unsuitable because of the time delay  
 CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue  
 CC plasminogen activator) may also be administered before, after or  
 CC simultaneously with the anti-CD18 antibody. Alternatively, the method can  
 CC be used to treat the third main type of ischemic stroke, systemic  
 CC hypoperfusion, e.g. resulting from cardiac arrest or drowning

XX Sequence 450 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 450;  
 Best Local Similarity 77.0%; Pred. No. 8.6e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYIHVWRQAPGKGLEWVASINPDYDITNY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYTMHWRQAPGKGLEWVASINPDYDITNY 60  
 QY 61 NORPKGRFTISLDKSKRTAYLQNSLRAPETAVYYCASHWIS-----DFPDYWGQGLTV 113  
 DB 61 NORPKGRFTISLDKSKRTAYLQNSLRAPETAVYYCASHWIS-----DFPDYWGQGLTV 120

QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

RESULT 14  
 AAY08755  
 ID AAY08755 standard; protein; 450 AA.

XX AAY08755;  
 XX 10-AUG-1999 (first entry)  
 XX Human IgG2 huH52 heavy chain protein fragment.

KM IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;  
 KM IgG4; kappa-CL domain; lambda-CL domain; focal ischemic stroke;  
 KM cerebroprotective; cerebral artery obstruction; blood flow; infarct;  
 KM CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;  
 KM antibody; huH52; heavy chain.

OS Homo sapiens.  
 XX US5914112-A.  
 XX 22-JUN-1999.  
 XX 22-JAN-1997; 97US-00788800.  
 XX 23-JAN-1996; 96US-0093038P.

PA (GETH ) GENENTECH INC.  
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

PI Thomas GR, Bednar MM, Gross CE;

DR WPI; 1999-370483/31.

XX Anti-CD18 antibodies in stroke.

PS Disclosure; Col 31-34; 25pp; English.

XX This invention describes a method for improving the clinical outcome in  
 CC focal ischemic stroke by administering novel anti-CD18 antibody which  
 CC has cerebroprotective properties. The invention particularly describes a  
 CC method of treating focal ischemic stroke caused by the obstruction of a  
 CC main cerebral artery which comprises administering an anti-CD18 antibody  
 CC to increase the blood flow or reduce the infarct size, where: (1) the  
 CC antibody binds to an extracellular domain of CD18 and inhibits or reduces  
 CC the ability of the cell expressing CD18 to bind to endothelium, (2) the  
 CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the  
 CC antibody dissociates CD11b/CD18 complex. This sequence represents the  
 CC human IgG 2 huH52 heavy chain region

XX Sequence 450 AA;

Query Match 78.8%; Score 499.5; DB 2; Length 450;  
 Best Local Similarity 77.0%; Pred. No. 8.6e-39;  
 Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYIHVWRQAPGKGLEWVASINPDYDITNY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYYTMHWRQAPGKGLEWVASINPDYDITNY 60  
 QY 61 NORPKGRFTISLDKSKRTAYLQNSLRAPETAVYYCASHWIS-----DFPDYWGQGLTV 113  
 DB 61 NORPKGRFTISLDKSKRTAYLQNSLRAPETAVYYCASHWIS-----DFPDYWGQGLTV 120

QY 114 TVSSAS 119  
 DB 121 TVSSAS 126

RESULT 15  
 ABG31890  
 ID ABG31890 standard; peptide; 450 AA.

XX ABG31890;  
 XX 05-NOV-2002 (first entry)

XX Full length humanised H52 antibody (huH52), heavy chain.

KM Human; humanised H52 antibody; huH52; cerebral blood flow; infarct size;  
 KM focal ischemic stroke; main cerebral artery;  
 KM tissue plasminogen activator; anti-CD18 antibody; stroke;  
 KM acute ischemic stroke; thrombolytic therapy;  
 KM Fabryb salvage receptor binding epitope; thromboembolic stroke.

XX Homo sapiens.  
 OS Synthetic.  
 XX US2002081294-A1.

XX 27-JUN-2002.  
 XX 20-DEC-2000; 2000US-00811384.  
 XX 23-JAN-1996; 96US-0093038P.  
 XX 22-JAN-1997; 97US-00788800.  
 XX 17-FEB-1999; 99US-00251652.

PA (GETH ) GENENTECH INC.

PI Bednar MM, Gross CE, Thomas GR, Gross LJ;

DR WPI; 2002-626528/67.

XX Increasing cerebral blood flow and/or reducing infarct size in focal  
 PT ischemic stroke using anti-CD18 antibody and tissue plasminogen activator  
 XX is useful to improve clinical outcome in acute ischemic stroke.

PS Disclosure; Page 6; 27pp; English.



CC The invention relates to a method of increasing cerebral blood flow and/  
 CC or reducing infarct size in focal ischaemic stroke caused by obstruction  
 CC of a main cerebral artery in a human, comprising co-administering tissue  
 CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the  
 CC stroke. The method is used to improve the clinical outcome in acute  
 CC ischaemic stroke and to provide an alternative to thrombolytic therapy  
 CC for treating thromboembolic stroke, particularly where thrombolytic  
 CC therapy has been unsuccessful or is contra-indicated. The present  
 CC sequence represents the full length humanised H52 antibody (huH52), heavy  
 CC chain used in the method of the invention

XX  
 SQ Sequence 450 AA;

Query Match 78.8%; Score 499.5; DB 5; Length 450;  
 Best Local Similarity 77.0%; Pred. No. 8,6e-39;

Matches 97; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY	1	EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIMHVRQAPGKGLEWVASINPDYDITNY	60
DB	1	EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIMHVRQAPGKGLEWVASINPDYDITNY	60
QY	61	NQRFKGRFTISLDKSKRTAYLQMSLRADTAIVYCAHWIS-----DFPDYWGQGLV	113
DB	61	NQRFMDRFTISVDKSTAYMQMNSLRADTAIVYCAWRGILNGFDVRYFPDVMGQGLV	120
QY	114	TVSSAS	119
DB	121	TVSSAS	126

Search completed: December 29, 2004, 19:35:44  
 Job time : 125.575 secs

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